

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 9, 2003, 18:42:23 : Search time 2626 Seconds
(without alignments)
7270.160 Million cell updates/sec

Title: US-10-060-066-2

Perfect score: 656

Sequence: 1 taagtctcaactgcacact.....tgttatctttatctcttg 656

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

- Database :
- 1: GenEmbl:*
 - 2: gb_ba:*
 - 3: gb_bt:*
 - 4: gb_in:*
 - 5: gb_ov:*
 - 6: gb_ov:*
 - 7: gb_ov:*
 - 8: gb_ov:*
 - 9: gb_ov:*
 - 10: gb_ov:*
 - 11: gb_ov:*
 - 12: gb_ov:*
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 - 14: gb_ov:*
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 - 37: gb_ov:*
 - 38: gb_ov:*
 - 39: gb_ov:*
 - 40: gb_ov:*
 - 41: gb_ov:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------|
| 1 | 597.8 | 90.4 | 185839 | 2 | AC079557 Mus muscu |
| 2 | 525 | 80.0 | 178910 | 2 | AC114434 Mus muscu |
| 3 | 387.4 | 59.1 | 1380 | 10 | AF361350 Mus muscu |
| 4 | 361.6 | 55.1 | 142388 | 2 | AC128446 Rattus no |
| 5 | 297.8 | 45.4 | 169997 | 2 | AC008440 Homo sapi |
| 6 | 269.8 | 41.1 | 1266 | 10 | AF361346 Rattus no |
| 7 | 236 | 36.0 | 190210 | 2 | AC022318 Homo sapi |
| 8 | 232.2 | 35.4 | 1386 | 9 | AF361354 Homo sapi |
| 9 | 191.2 | 29.1 | 633 | 9 | AF234892 Homo sapi |
| 10 | 171 | 26.1 | 1281 | 9 | AF288388 Homo sapi |
| 11 | 158.4 | 24.1 | 142388 | 2 | AC128446 Rattus no |
| 12 | 92 | 14.0 | 987 | 5 | AY037891 Gallus ga |
| 13 | 86.4 | 13.2 | 720 | 9 | HSCACNG1 |
| 14 | 86.4 | 13.2 | 984 | 6 | AR165149 Sequence |
| 15 | 86.4 | 13.2 | 984 | 6 | AX101260 Sequence |
| 16 | 86.4 | 13.2 | 984 | 10 | AF361341 Rattus no |
| 17 | 86.4 | 13.2 | 984 | 10 | MMU272045 Mus muscu |
| 18 | 86.4 | 13.2 | 1001 | 9 | AF162692 Homo sapi |
| 19 | 86.4 | 13.2 | 3392 | 9 | BC034532 Homo sapi |
| 20 | 86.4 | 13.2 | 94538 | 10 | AL645853 Mouse DNA |
| 21 | 86.4 | 13.2 | 173126 | 9 | AC005988 Homo sapi |
| 22 | 83.2 | 12.7 | 1071 | 6 | AR202726 Sequence |
| 23 | 75.4 | 11.5 | 209887 | 2 | AC079424 Mus muscu |
| 24 | 62.8 | 9.6 | 58937 | 2 | AC129819 Rattus no |
| 25 | 62.4 | 9.5 | 1548 | 5 | AF118819 Gallus ga |
| 26 | 58.6 | 8.9 | 125020 | 9 | AF429315 Homo sapi |
| 27 | 54.6 | 8.3 | 12667 | 2 | AC015839 Homo sapi |
| 28 | 54.4 | 8.3 | 972 | 9 | AF096322 Homo sapi |
| 29 | 54.4 | 8.3 | 99497 | 9 | HS293166 Human DNA |
| 30 | 53.6 | 8.2 | 948 | 10 | AF361340 Rattus no |
| 31 | 53.6 | 8.2 | 948 | 10 | MMU272044 Mus muscu |
| 32 | 53.6 | 8.2 | 1477 | 6 | AR202725 Sequence |
| 33 | 53.6 | 8.2 | 130440 | 2 | AC130391 Rattus no |
| 34 | 53.6 | 8.2 | 187780 | 2 | AC094178 Rattus no |
| 35 | 53.2 | 8.1 | 63082 | 2 | AC022663 Homo sapi |
| 36 | 52.8 | 8.0 | 972 | 10 | AF361339 Rattus no |
| 37 | 52.8 | 8.0 | 1124 | 10 | AF118818 Rattus no |
| 38 | 52.8 | 8.0 | 1554 | 10 | AF077739 Mus muscu |
| 39 | 52.8 | 8.0 | 1558 | 6 | AR202724 Sequence |
| 40 | 52.8 | 8.0 | 155833 | 2 | AC120678 Rattus no |
| 41 | 52.8 | 8.0 | 197660 | 10 | AL589650 Mouse DNA |
| 42 | 52.8 | 8.0 | 208651 | 10 | AC090493 Genomic s |
| 43 | 52 | 7.9 | 948 | 9 | AF100346 Homo sapi |
| 44 | 52 | 7.9 | 1012 | 9 | AF134640 Homo sapi |
| 45 | 52 | 7.9 | 2092 | 9 | AK054543 Homo sapi |

ALIGNMENTS

RESULT 1
AC079557/c 185839 bp DNA linear HTG 02-SEP-2000
LOCUS Mus musculus clone RP23-449F12, WORKING DRAFT SEQUENCE, 16
DEFINITION unordered pieces.
ACCESSION AC079557
VERSION AC079557.1 GI:9964922
KEYWORDS HTG: HTGS_PHASE1; HTGS_DRAFT.
SOURCE Mus musculus.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 185839)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Mouse

| | |
|-----------|--|
| JOURNAL | Unpublished |
| REFERENCE | 2 (bases 1 to 185839) |
| AUTHORS | DOE Joint Genome Institute. |
| TITLE | Direct Submission |
| JOURNAL | Submitted (02-SEP-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA |
| COMMENT | -----Genome Center |

```
web site: http://www.jgl.doe.gov
-----
Project Information
Center Project Name: 1909420
Center clone name: RPCI-23_449F12
```

Summary Statistics

| | |
|------------------------|--|
| Consensus quality: | 172503 bases at least Q40 |
| Consensus quality: | 177768 bases at least Q30 |
| Consensus quality: | 179073 bases at least Q20 |
| Consensus insert size: | 187000; agarose-tp estimation |
| Estimated insert size: | 184339; sum-of-contigs estimation |
| Quality coverage: | 7.81 ln Q20 bases; agarose-tp estimation |
| Quality coverage: | 7.93 ln Q20 bases; sum-of-contigs estimation |

```
* NOTE: This is a 'working draft' sequence. It currently
* consists of 16 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of 'N', but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
```

| | | | |
|---|---------|---------|------------------------------|
| * | 1 | 1081: | contig of 1081 bp in length |
| * | 1082 | 1181: | gap of unknown length |
| * | 1182 | 4298: | contig of 3117 bp in length |
| * | 4298 | 4398: | gap of unknown length |
| * | 4398 | 6732: | contig of 2334 bp in length |
| * | 6733 | 6832: | gap of unknown length |
| * | 6833 | 11628: | contig of 4794 bp in length |
| * | 11627 | 11726: | gap of unknown length |
| * | 11727 | 15545: | contig of 3819 bp in length |
| * | 15546 | 15645: | gap of unknown length |
| * | 15646 | 20007: | contig of 4362 bp in length |
| * | 20008 | 20107: | gap of unknown length |
| * | 20108 | 26155: | contig of 6049 bp in length |
| * | 26157 | 26256: | gap of unknown length |
| * | 26257 | 32958: | contig of 6702 bp in length |
| * | 32959 | 33059: | gap of unknown length |
| * | 33059 | 42014: | contig of 8956 bp in length |
| * | 42015 | 42114: | gap of unknown length |
| * | 42115 | 50688: | contig of 8574 bp in length |
| * | 50689 | 50788: | gap of unknown length |
| * | 50789 | 61298: | contig of 10510 bp in length |
| * | 61299 | 61398: | gap of unknown length |
| * | 61399 | 77262: | contig of 15871 bp in length |
| * | 77270 | 77363: | gap of unknown length |
| * | 77370 | 95693: | contig of 18324 bp in length |
| * | 95694 | 95793: | gap of unknown length |
| * | 119999: | 119999: | contig of 24206 bp in length |
| * | 120000 | 120097: | gap of unknown length |
| * | 120100 | 150277: | contig of 30174 bp in length |
| * | 150274 | 150373: | gap of unknown length |
| * | 150374 | 185888: | contig of 35466 bp in length |

FEATURES
SOURCE

Location/Qualifiers
1. .185839

| BASE COUNT | | | | | |
|------------|---|-------|---|-------|-------------|
| 48719 | a | 43498 | c | 42466 | g |
| | | | | 49655 | t |
| | | | | | 1501 others |

| | | | | |
|-----------------------|--------|---------------------|-------|---------------|
| Query Match | 90.48; | Score 592.8; | DB 2; | Length 185839 |
| Best Local Similarity | 95.38; | Pred. NO. 2.7e-127; | | |

Matches 625; Conservative 0; Mismatches 29; Indels 2; Gaps 2;

| LOCUS | DEFINITION | ACCESSION | VERSION | KEYWORDS | SOURCE | ORGANISM | REFERENCE | AUTHORS |
|------------|--|---|---------|----------|-----------------|----------|-----------|---------|
| Oy | 1 | TATGCTTCACCTCTGACCTTCGCTCTGACACACACCTGCTGTCGCCGCCGCCGCCCTTC | 60 | | | | | |
| Db | 57586 | TATGCTTCACCTCTGACCTTCGCTCTGACACACACCTGCTGTCGCCGCCGCCGCCCTTC | 57528 | | | | | |
| Oy | 61 | TGGCCCTTGAGGCCCCCAGCTTCTGCTGTCGTGTATGCCGCCGCCGCCGCCGCCGCCG | 120 | | | | | |
| Db | 57527 | TGGCCCTTGAGGCCCCCAGCTTCTGCTGTCGTGTATGCCGCCGCCGCCGCCGCCGCCG | 57468 | | | | | |
| Oy | 121 | CCCGGCTCCGCTGTCGCCGCTGTGGCCCGAGGGCCCCCGGGTGGCCAGTGGTGAACCTGG | 180 | | | | | |
| Db | 57467 | CCCGGCTCCGCTGTCGCCGCTGTGGCCCGAGGGCCCCCGGGTGGCCAGTGGTGAACCTGG | 57408 | | | | | |
| Oy | 181 | AGTCATTGAAACGCTGGAATGAAAGAGAGGGCTTTGTGTGTGTAAGAAAGGGCGTTACGTAAC | 240 | | | | | |
| Db | 57407 | AGTCATTGAAACGCTGGAATGAAAGAGAGGGCTTTGTGTGTGTAAGAAAGGGCGTTACGTAAC | 57348 | | | | | |
| Oy | 241 | TACTACACCAACCTGCGGCGCTTTCGCGGCTTTTGGGCTCATGTACATCGGCATCAGACATG | 300 | | | | | |
| Db | 57347 | TACTACACCAACCTGCGGCGCTTTCGCGGCTTTTGGGCTCATGTACATCGGCATCAGACATG | 57288 | | | | | |
| Oy | 301 | ACTACGGGCTACACCAAGAGCTCTCATCTGTGCAACACCAACCTCAGACAGAGTGATG | 360 | | | | | |
| Db | 57287 | ACTACGGGCTCTACACCAAGAGCTCTCATCTGTGCAACACCAACCTCAGACAGAGTGATG | 57228 | | | | | |
| Oy | 361 | ACGGACCAACCCCATCGTGGGGGACAGTGGCTCTCCGAGAGAAGAACCCCTGGGGGCTTCA | 420 | | | | | |
| Db | 57227 | ACGGACCAACCCCATCGTGGGGGACAGTGGCTCTCCGAGAGAAGAACCCCTGGGGGCTTCA | 57168 | | | | | |
| Oy | 421 | CACATTTCAGGCTCTGCGGCGATATGCTGCTGTGGAAAGTGGGTGCAGAAAGGCCCTGGCT | 480 | | | | | |
| Db | 57167 | CACATTTCAGGCTCTGCGGCGATATGCTGCTGTGGAAAGTGGGTGCAGAAAGGCCCTGGCT | 57108 | | | | | |
| Oy | 481 | GGCCACCTCCGWTGAAGCCTGTGCTTCACGCAATCGACTTATGATGTCTGAGTCTCAA | 540 | | | | | |
| Db | 57107 | GGCCACCTCCGWTGAAGCCTGTGCTTCACGCAATCGACTTATGATGTCTGAGTCTCAA | 57048 | | | | | |
| Oy | 541 | CCCAAGGCTTGAAGGGGTGCTTTACGCTGTGAGAGCGGTATTCATATGACACCCCTCCA | 600 | | | | | |
| Db | 57047 | CCCAAGGCTTGAAGGGGTGCTTTACGCTGTGAGAGCGGTATTCATATGACACCCCTCCA | 56988 | | | | | |
| Oy | 601 | TGCTCTGTTACAAATCCCTCTCTGGGAGTATGATGTTATTTTATTTTCTCTTGG | 656 | | | | | |
| Db | 56987 | TGCTCTGTTACAAATCCCTCTCTGGGAGTATGATGTTATTTTATTTTATTTACTGG | 56933 | | | | | |
| RESULT 2 | | | | | | | | |
| AC114434/C | AC114434 | 178910 bp | DNA | linear | HTG 13-JUL-2001 | | | |
| LOCUS | Rattus norvegicus clone CH230-210c18, *** SEQUENCING IN PROGRESS | | | | | | | |
| DEFINITION | ***, 60 unordered pieces. | | | | | | | |
| ACCESSION | AC114434 | | | | | | | |
| VERSION | AC114434.2 | GI:21737492 | | | | | | |
| KEYWORDS | HTG; HTGS; PHASE1. | | | | | | | |
| SOURCE | Norway rat. | | | | | | | |
| ORGANISM | Rattus norvegicus | | | | | | | |
| | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; | | | | | | | |
| | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; | | | | | | | |
| | Rattus. | | | | | | | |
| REFERENCE | 1 (bases 1 to 178910) | | | | | | | |
| AUTHORS | Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., | | | | | | | |
| | Alsbrooks,S.L., Amaralunge,H.C., Are,J.R., Ayele,M., Banks,T., | | | | | | | |
| | Barbarta,J., Benton,J., Blimage,K., Blankenburg,K., Bonin,D., | | | | | | | |
| | Bouck,J., Bowle,S., Brileva,M., Brown,E., Brown,M., Bryant,N.P., | | | | | | | |
| | Bunyah,C., Butch,P., Butkelt,C., Butrell,K.L., Byrd,N.C., | | | | | | | |
| | Carroll,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., | | | | | | | |
| | Chen,G., Chen,R., Chen,Z., Chowdhury,I., Christopoulos,C., | | | | | | | |
| | Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., | | | | | | | |
| | Dayla,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A., | | | | | | | |
| | DeJaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H., | | | | | | | |
| | Douthett,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., | | | | | | | |
| | Einhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escoto,M., | | | | | | | |

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| 3256 | 3425: | contig of 1070 bp in length |
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| 3326 | 4946: | contig of 1421 bp in length |
| 4947 | 5046: | gap of unknown length |
| 5047 | 6176: | contig of 1130 bp in length |
| 6177 | 6276: | gap of unknown length |
| 6277 | 7401: | contig of 1125 bp in length |
| 7402 | 7501: | gap of unknown length |
| 7502 | 9003: | contig of 1502 bp in length |
| 9004 | 9103: | gap of unknown length |
| 9104 | 10577: | contig of 1474 bp in length |
| 10578 | 10677: | gap of unknown length |
| 10678 | 11978: | contig of 1301 bp in length |
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| 12079 | 13339: | contig of 1251 bp in length |
| 13330 | 13429: | gap of unknown length |
| 13430 | 14761: | contig of 1332 bp in length |
| 14762 | 14861: | gap of unknown length |
| 14862 | 16134: | contig of 1273 bp in length |
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| 53489 | 55386: | gap of unknown length |
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| 56197 | 56296: | gap of unknown length |
| 56297 | 58044: | contig of 1748 bp in length |
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| 58145 | 59881: | contig of 1737 bp in length |
| 59882 | 62212: | contig of 2231 bp in length |
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| 62313 | 65054: | contig of 2742 bp in length |
| 65055 | 65154: | gap of unknown length |
| 65155 | 67490: | contig of 2336 bp in length |

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* 67591 67590: gap of unknown length
* 70538 70538: contig of 2948 bp in length
* 70639 70638: gap of unknown length
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* 73043 73042: gap of unknown length
* 76294 76294: contig of 3252 bp in length
* 76395 76394: gap of unknown length
* 79038 79037: contig of 2643 bp in length
* 82946 82946: contig of 3809 bp in length
* 83047 83046: gap of unknown length
* 85708 85707: contig of 2661 bp in length
* 85808 85807: gap of unknown length
* 87649 87648: contig of 1841 bp in length
* 87749 87748: gap of unknown length
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* 91863 91862: gap of unknown length
* 95722 95721: contig of 3859 bp in length
* 95822 95821: gap of unknown length
* 99307 99306: contig of 3485 bp in length
* 99407 99406: gap of unknown length
* 103927 103926: contig of 4520 bp in length
* 104027 104026: gap of unknown length
* 109478 109477: contig of 5451 bp in length
* 109578 109577: gap of unknown length
* 114509 114509: contig of 4832 bp in length
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* 119171 119171: contig of 4662 bp in length
* 119172 119171: gap of unknown length
* 119272 126347: contig of 7076 bp in length
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Query Match
Best Local Similarity 93.5%; Score 525; DB 2; Length 178910;
Matches 565; Conservative 0; Mismatches 37; Indels 2; Gaps 2;

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Db 160474 GGGCCCTGAGGCCCCAGCTTCTGCTGATCCGCCCCAGCCGCGCACGGC 160415
122 CCGCCCTCGCTGCGCCGGTGTGCGCCAGCGCCCGCGTTGCCAGTGTGAAC 181
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Db 160114 ACATTCAGGCTCTGCGGATATGCTGCTGGAAGGTAGGAGGAGCGCTGGTGTG 160055
482 GCGACCTCCGNTGAAAGCTGTGCTTCACAAATCGATTNAGTGTGAGTCTCAAC 541
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Db 160054 GCGACCTCCGNTGAAAGCTGTGCTTCACAAATCGATTNAGTGTGAGTCTCAAC 159995
542 CCAAGGCTTGAAGGGTGTGCTTACTGCTGAGAGCG- GNTAATTCATGACACCTCCA 600
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Db 159994 CCAAGGCTTGAAGGGTGTGCTTACTGCTGAGAGAGCTATGATTCATGATCCCTCTG 159935
QY 601 TNCC 604
111
Db 159934 TCCC 159931

RESULT 3
AF361350
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL

AF361350 1380 bp mRNA linear ROD 21-DEC-2001
(Caen98) mRNA, complete cds.
AF361350
AF361350.1 GI:17974533
Mus musculus.
Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1380)
Chu, P.-J., Robertson, H.M. and Best, P.M.
Calcium channel gamma subunits provide insights into the evolution
of this gene family
Gene 280 (1-2), 37-48 (2001)
21601102
11738816
2 (bases 1 to 1380)
Chu, P.-J., Robertson, H. and Best, P.M.
Direct Submission
Submitted (14-MAR-2001) Department of Molecular and Integrative
Physiology, University of Illinois, 407 S. Goodwin Ave., Urbana, IL
61801, USA

FEATURES
source
Location/Qualifiers
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INHPEDPDYHDSNEYILRYVRASITPIISAILLLGCVASRYKSKRNILIG
AGILVNAAGLSNITIGVIVISNMGEPKRDDEKKNHYSTGWSYFEGLSITLAEVI
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BASE COUNT
ORIGIN
Query Match
Best Local Similarity 99.7%; Score 387.4; DB 10; Length 1380;
Matches 388; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Oy 249 ACCATCGGCGCTTTCGGGCTTTGGCCCTCATGACCATCGCATGACGACTGACTG 308
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Oy 309 CTTACACAGAGCTCTGATCTGCAACACACCACTCAGACGAGTGATGACGAGCA 368
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Oy 369 CCCCATCTGGGGGCGAGTGGCTCCCTCCGAGAGAAGACCTGGGGGCTCAGACATTC 428
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RESULT 4
AC128446/c
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DEFINITION Rattus norvegicus clone CH230-95B19, *** SEQUENCING IN PROGRESS
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***, 67 unordered pieces.
AC128446
VERSION AC128446.1 GI:21909138
KEYWORDS HTG: HTGS, PHASE1.
SOURCE Rattus norvegicus.
ORGANISM Rattus norvegicus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 142388)
Muzny,D.M., Adams,C., Adio-Oduola,B., Alifosman,F.R., Allen,C.,
Alshrooke,S.L., Amaratunga,H.C., Are,J.R., Ayale,M., Banks,T.F.,
Barbata,J., Benton,J., Bimaga,K., Blankenburg,K., Bonnin,D.,
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Carroll,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
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Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
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Meheswar,M., Mapua,P., Martin,R., Meadorale,A., Martinez,E.,
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Oregunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
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Scherrer,S., Scott,G., Shen,H., Shooshitari,N., Sisson,I.,
Soedjaren,E., Sonalke,T., Sparks,A., Stanley,H., Stone,H.,
Sulton,A., Svatek,A., Taber,P., Tamerisa,A., Tamerisa,K., Tang,H.,
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Uman,K., Vasquez,L., Vera,V., Villalob,D., Vinson,R., Wang,O.,
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Weinstock,G. and Gibbs,R.
TITLE
JOURNAL
Unpublished

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REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
2 (bases 1 to 142388)
Mortley,K.C.
Direct Submission
Submitted (19-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GWS
Center clone name: CH230-95B19
----- Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 77782 bases at least Q40
Consensus quality: 85255 bases at least Q30
Consensus quality: 89224 bases at least Q20
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* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank-draft-data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 67 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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1022 1121: gap of unknown length
1122 1229: contig of 1176 bp in length
1229 2297: gap of unknown length
2298 2398: contig of 1416 bp in length
2398 3814: gap of unknown length
3814 5197: contig of 1284 bp in length
5197 5297: gap of unknown length
5298 6342: contig of 1044 bp in length
6342 6442: gap of unknown length
6442 7746: contig of 1305 bp in length
7746 7847: gap of unknown length
7847 9653: contig of 1807 bp in length
9653 9754: gap of unknown length
9754 11431: contig of 1678 bp in length
11431 11532: gap of unknown length
11532 12797: contig of 1265 bp in length
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15277 15377: gap of unknown length
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16423 16523: gap of unknown length
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16524 18113: contig of 1592 bp in length
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18215 18216: gap of unknown length
18216 19345: contig of 1130 bp in length
19345 21241: gap of unknown length
21241 21341: contig of 1796 bp in length
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22496 22596: gap of 1155 bp in length
22596 23853: contig of 1257 bp in length
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23954 25776: contig of 1823 bp in length
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25877 26990: contig of 1114 bp in length
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28279 29410: contig of 1131 bp in length

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| 29911 | 31147: | contig of | 1637 | bp in length |
| 31148 | 31247: | gap of | unknown | length |
| 31248 | 32473: | contig of | 1226 | bp in length |
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| 32574 | 34652: | contig of | 2079 | bp in length |
| 34653 | 34752: | gap of | unknown | length |
| 34753 | 36601: | contig of | 1849 | bp in length |
| 36602 | 36701: | gap of | unknown | length |
| 36702 | 38125: | contig of | 1424 | bp in length |
| 38126 | 38225: | gap of | unknown | length |
| 38226 | 39774: | contig of | 1549 | bp in length |
| 39775 | 39874: | gap of | unknown | length |
| 39875 | 41034: | contig of | 1160 | bp in length |
| 41035 | 41154: | gap of | unknown | length |
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| 42834 | 42933: | gap of | unknown | length |
| 42934 | 44167: | contig of | 1234 | bp in length |
| 44168 | 44267: | gap of | unknown | length |
| 44268 | 45446: | contig of | 1179 | bp in length |
| 45447 | 45546: | gap of | unknown | length |
| 45547 | 47410: | contig of | 1864 | bp in length |
| 47411 | 47510: | gap of | unknown | length |
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| 80748 | 83375: | gap of | unknown | length |
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| 83476 | 85478: | gap of | unknown | length |
| 85478 | 85578: | contig of | 2003 | bp in length |
| 85579 | 87528: | gap of | unknown | length |
| 87529 | 87628: | contig of | 1950 | bp in length |
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| 90681 | 90780: | contig of | 3052 | bp in length |
| 90781 | 93681: | gap of | unknown | length |
| 93682 | 93686: | contig of | 3066 | bp in length |
| 93687 | 93966: | gap of | unknown | length |
| 96843 | 96843: | contig of | 2877 | bp in length |
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| 100707 | 100706: | contig of | 3763 | bp in length |
| 100806 | 100806: | gap of | unknown | length |
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| Db 58613 | TTTTCCCGCTTTTGTGTGACCCCCCAGCCGCGGACCGGCCCGCCCTTTCGTGTGCCCGGT 58554 | | | |
| QY 142 | GGTGGCCCAACGGCCCCCGGTTGCTCAGTGTGTGAACCTGAGTTCATTTGAACGCTGAGATG 201 | | | |
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| QY 202 | AAGAAAGAGGCTTTGTGTGTGTGAAGGCGCTTCAGGTACTACTGACA-CCATGGCGCC 260 | | | |
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| QY 261 | TTCCGGGCGCTTTTGGCGCTATGACCATGTGCGCATTCAGCATCTGTGGCTCTACACAAGA 320 | | | |
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| QY 321 | GCTTCATCTGCAACACCAACCAACC-TCACAGCAGGTATACAGGACCCACCCATCTGTG- 378 | | | |
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| QY 379 | GGGGCAGTGTGCTCTCTCCAGAAAGAACCCCTGGGGCGCTACACATTCAGGCGCTTGCGC 438 | | | |
| Db 58314 | GGGGCAGTGTGCTCTCTCAAGAAAGAGACCTGGGGCGCTCACACATTCAGGCGCTTGCGC 58255 | | | |
| QY 439 | GGATATGTGCTGCTGGAAAGTATAGGTGCGAAGGAGCCCTGGGGCGCACCTCGGATGAAGC 498 | | | |
| Db 58254 | GGATATGCTGCTGCTGGAAGATAGGTGTGCGAAGAGGCCACGCTTGCCACCTCTCGGTGAAGC 58195 | | | |
| QY 499 | CTGTCCCTTCACCAAAATGCATTTAGTGTCTGAGTCTCAACCCAAAGNCTTGAGGGGT 558 | | | |
| Db 58194 | CTGTCCCTTCACCAAAAGGACGCTAGTGTCTGAAATCTCATCCCAAGCTCTTGAGGGGT 58135 | | | |
| QY 559 | GTGCTTTACTGTGTGAGGCG-GNATATTCATGTGACCCCTCATATNC 604 | | | |
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| AC008440 | 169997 bp | DNA | linear | PRI 13-JUL-2002 |
| LOCUS | AC008440 | | | |
| DEFINITION | Homo sapiens chromosome 19 clone CTC-331H23, complete sequence. | | | |
| ACCESSION | AC008440 | | | |
| VERSION | AC008440.9 | GI:21743728 | | |
| KEYWORDS | HTG. | | | |
| SOURCE | human. | | | |
| ORGANISM | Homo sapiens | | | |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| AUTHORS | Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. | | | |
| TITLE | 1 (bases 1 to 169997) | | | |
| JOURNAL | DOE Joint Genome Institute and Stanford Human Genome Center. | | | |
| REFERENCE | Unpublished | | | |
| AUTHORS | 2 (bases 1 to 169997) | | | |
| TITLE | DOE Joint Genome Institute. | | | |
| JOURNAL | Direct Submission | | | |
| REFERENCE | Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint | | | |
| AUTHORS | Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA | | | |
| TITLE | 3 (bases 1 to 169997) | | | |
| JOURNAL | DOE Joint Genome Institute and Stanford Human Genome Center. | | | |
| REFERENCE | Direct Submission | | | |
| AUTHORS | Submitted (01-JUN-2001) DOE Joint Genome Institute, 2800 Mitchell | | | |
| TITLE | Drive, Walnut Creek, CA 94598, USA | | | |
| JOURNAL | 4 (bases 1 to 169997) | | | |
| REFERENCE | DOE Joint Genome Institute and Stanford Human Genome Center. | | | |
| AUTHORS | Direct Submission | | | |
| TITLE | Submitted (13-JUL-2002) DOE Joint Genome Institute, 2800 Mitchell | | | |
| JOURNAL | Drive, Walnut Creek, CA 94598, USA | | | |
| REFERENCE | On Jul 13, 2002 this sequence version replaced gi:14277251. | | | |
| COMMENT | | | | |

| RESULT 9 | AF234892 | 633 bp | mRNA | linear | PRI 02-JAN-2002 |
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| LOCUS | AF234892 | | | | |
| DEFINITION | Homo sapiens putative voltage gated calcium channel gamma-8 subunit | | | | |
| ACCESSION | AF234892 | | | | |
| VERSION | AF234892.1 | | | | |
| KEYWORDS | | | | | |
| SOURCE | Homo sapiens. | | | | |
| ORGANISM | Homo sapiens. | | | | |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. | | | | |
| AUTHORS | 1 (bases 1 to 633) | | | | |
| TITLE | Black, J.L., III, Kryzer, T.J., and Lennon, V.A. | | | | |
| JOURNAL | Proposed Homo sapiens voltage-gated calcium channel gamma-6 subunit | | | | |
| REFERENCE | Unpublished | | | | |
| AUTHORS | 2 (bases 1 to 633) | | | | |
| TITLE | Black, J.L., III, Kryzer, T.J., and Lennon, V.A. | | | | |
| JOURNAL | Direct Submission | | | | |
| FEATURES | Submitted (15-FEB-2000) Department of Psychiatry and Psychology, Mayo Clinic, 200 SW 1st Street, Rochester, MN 55905, USA | | | | |
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| Db | 82 GTGCTGCTGAGAGAGGGTGGGGCGCTTCCGCCCTTCATATGACCATGCCATGCATCAGC | 141 | | | |
| QY | 297 ACTGACTACTGAGCTCTACACAAGAGCTCTCATCTGCAACACACCAACCTCACAGC--A | 353 | | | |
| Db | 142 ACTGACTACTGAGCTCTACACAAGAGCTCTCATCTGCAACACACCAACCTCACAGC | 201 | | | |
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| Db | 202 GGGCAGCAGCGGAGACCCCGCCACCGGGGGGGGGCGGCGCTCGGAGAAAGAGACCCCGGC | 261 | | | |
| QY | 414 GGCTCAGACATTCAGGCGCTTGGCGGATATGCTGCTCGAAGC | 457 | | | |
| Db | 262 GGCTCAGACATTCAGGCGCTTGGCGGATATGCTGCTCGAAGC | 305 | | | |
| RESULT 10 | AF288388 | 1281 bp | mRNA | linear | PRI 16-MAR-2001 |
| LOCUS | AF288388 | | | | |
| DEFINITION | Homo sapiens calcium channel gamma subunit 8 (CACNG8) mRNA, partial cds. | | | | |

| ACCESSION | AF288388 |
|---------------------------|--|
| VERSION | AF288388.1 |
| KEYWORDS | GI:13357179 |
| SOURCE | |
| ORGANISM | Homo sapiens. |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. |
| AUTHORS | 1 (bases 1 to 1281) |
| TITLE | Burgess,D.L., Gefrides,L.A., Foreman,P.J. and Noebels,J.L. A cluster of three novel Ca2+ channel gamma subunit genes on chromosome 19q13.4: evolution and expression profile of the gamma subunit gene family Genomics 71 (3), 339-350 (2001) |
| JOURNAL | |
| MEDLINE | 1170751 |
| PUBMED | 2 (bases 1 to 1281) |
| REFERENCE | Burgess,D.L., Gefrides,L.A., Foreman,P.J. and Noebels,J.L. Direct Submission Submitted (20-JUL-2000) Neurology, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA |
| JOURNAL | |
| FEATURES | location/Qualifiers |
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| Query Match | 26.1%; Score 171; DB 9; Length 1281; |
| Best Local Similarity | 82.9%; Pred. No. 2,4e-29; |
| Matches 208; Conservative | 0; Mismatches 40; Indels 3; Gaps 1; |
| Oy | 210 GATTGTGGTGGAAGAGGGCGTTGAGGATCAGACACCACCATCGGCCTTCGGGGCT 269 |
| Dd | 1 GGCCCTCTGGTGGCAAGAGGGGTGCAGAGTGCTGACGACGCGTGGCGGCCCTTCGCCGCC 60 |
| Oy | 270 TTTGGCTCATGACCATCGCCATCAGACACTGACTACTGGCTCTACACAAGACTCTCATC 329 |
| Dd | 61 TTGCGCTCATGATGACCATCGCCATCAGCACTGACTACTGGCTCTACACGCGCGCCTCATC 120 |
| Oy | 330 TGCACACCAACCAACTCAGAC---AGTGATGACAGACACACCCCCTATGTTGGGGCACT 386 |
| Dd | 121 TGCAACACCAACCACTCAGCGCGGGCGGACGACGGGAGCCCCCACCACGCGGGGGCGGG 180 |
| Oy | 387 GGCCTCTCGAAGAAAGACCCCTGGGGGCTCACAACATTCAGCGCTCGGCGGATATGC 446 |
| Dd | 181 GGGCGCTCGAGAAAGAACGCCCGCGGCTCTACGCACTCGGGGCTCTGGAGAGATCTCG 240 |
| Oy | 447 TGCCTGGAAG 457 |
| Dd | 241 TGCTGTGAAG 251 |
| RESULT 11 | |
| LOCUS | AC128446 14238 bp DNA linear HTG 19-JUL-2002 |

| | |
|------------|---|
| DEFINITION | Rattus norvegicus clone CH230-95B19, *** SEQUENCING IN PROGRESS |
| ACCESSION | AC128446 |
| VERSION | 1 |
| KEYWORDS | HTG; HTGS; PHASE1. |
| SOURCE | Rattus norvegicus. |
| ORGANISM | Rattus norvegicus |
| REFERENCE | Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. |
| AUTHORS | 1 (bases 1 to 142388) |
| | Munzy,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaralunge,H.C., Are,J.R., Ayale,M., Banks,T., Barbara,J., Benton,J., Bilmage,K., Blankenburg,K., Bonnin,D., Bowick,J., Bowie,S., Brileva,M., Brown,E., Brown,M., Bryant,L.N.P., Buhay,C., Burck,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carton,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinb,H.H., Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Dublin,K.J., Earhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,U.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B., Homsi,F., Howard,S., Huber,J., Huijck,S., Hume,D., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudas,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C., Kratochic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L., Li,J., Li,Z., Licharge,O., Lieu,C., Liu,J., Liu,W., Lounsged,H., Lozadó,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E., Massey,E., Mahoney,E., McLeod,M.P., Meador,M., Mel,G., Metzker,S., Minter,G., Minter,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S., Moser,M., Neel,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nkwenkwo,S., Ogun,M., Okunnu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Rivers,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shooshani,N., Sisson,I., Sodereen,E., Sonalke,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Stratik,A., Tabot,P., Tamerisa,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C., Taylor,T., Telirod,B., Thomas,N., Thomas,S., Usmani,K., Vasquez,L., Ver,V., Villison,D., Vinsion,R., Wang,Q., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williams,G., Williams,A., Wleczek,R., Wooten,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorilla,S., Nelson,D., Weinstock,G. and Gibbs,R. |
| TITLE | Direct Submission |
| JOURNAL | Unpublished |
| REFERENCE | 2 (bases 1 to 142388) |
| AUTHORS | Worley,K.C. |
| TITLE | Direct Submission |
| JOURNAL | Submitted (19-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA |
| COMMENT | ----- Genome Center Center: Baylor College of Medicine Center code: BCM Web site: http://www.hgsc.bcm.tmc.edu/ Contact: hgsc-help@bcm.tmc.edu ----- Project Information Center project name: GWS Center clone name: CH230-95B19 ----- Summary Statistics Sequencing vector: Plasmid: Assembly program: Phrap: version 0.990339 Consensus quality: 85255 bases at least Q40 |

RESULT 12
LOCUS AY037891 987 bp mRNA linear VRT 01-APR-2002
DEFINITION Gallus gallus calcium channel gamma 4 subunit (CACNG4) mRNA,
complete cds.
ACCESSION AY037891
VERSION AY037891.1 GI:15418940
KEYWORDS
SOURCE
ORGANISM Gallus gallus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE
AUTHORS 1 (bases 1 to 987)
Kious,B.M., Baker,C.V., Bronner-Fraser,M. and Knecht,A.K.
TITLE Identification and characterization of a calcium channel gamma
subunit expressed in differentiating neurons and myoblasts
JOURNAL Dev. Biol. 243 (2), 249-259 (2002)
MEDLINE 21881550
PUBMED 11884034
REFERENCE
AUTHORS 2 (bases 1 to 987)
Kious,B.M., Bronner-Fraser,M. and Knecht,A.K.
TITLE Direct Submission
JOURNAL Submitted (04-JUN-2001) Biology, Caltech, Mail Code 139-74,
Pasadena, CA 91125, USA
FEATURES
source 1..987
location/Qualifiers
/organism="Gallus gallus"
/db_xref="taxon:9031"
1..987
/gene="CACNG4"
1..987
/gene="CACNG4"
/codon_start=1
/product="calcium channel gamma 4 subunit"
/protein_id="AAK72510.1"
/db_xref="GI:15418941"
/translation="MVMCDRGVOMLLTTVGAFPAFSLMAIAGTDYMLYSAHICNGT
NITDDDGPPKRGKAGDLTHSLMRLICCELEGYGHCRINHPEDNDYDHSRYLL
RIVRASSYFPLISLILLGLGICVAGAGIVSKNITLISACILVAASLTNIGLIT
ISSNAGDPSDKRDEKDKHNYGMSFTGALSIFYAETIGLVANITYEKNELREKT
KREFLKTSSSPVAMPSPYRYRRRSRSSSTSPSRDISPVGMLASTITPMEIS
MYLSREPLKVTYTAASYNADQDASFLQVHNFLOKEFKELHVMVNRRTTVV"
BASE COUNT 264 a 261 c 240 g 222 t
ORIGIN
Query Match 14.0%; Score 92; DB 5; Length 987;
Best Local Similarity 65.9%; Pred. No. 5.3e-11;
Matches 162; Conservative 0; Mismatches 60; Indels 24; Gaps 1;
QY 214 TGTGGTGAAGAAAGGGCGTTGAGTACTGACCAACCATGGCGGCTTGGGGCTTTG 273
DB 5 TGTGGTGAACCGTGGCGTGCAGATGCTGACCAACGGTGGAGCTTTCGGCGCTTCA 64
QY 274 GCGTCATGACATCGCATCAGCACTGATGAGTACTGCTTACACAAGAGCTTCATCTGCA 333
DB 65 GCGTCATGCGCATTCGCGCATCGGTACCGACTACTGGCTGATCTCAGCGGCACATCTGCA 124
QY 334 ACACCAACCACTCAGCAGCAGTATGACGACACACCCCATGCTGGGGGCACTGCTCT 393
DB 125 ACGGACCAACATCAGACGAGGATACGACAGGGGCC----- 163
QY 394 CCGAAGAAGAGACCTGGGGGCTCAGCATTCAGGCGCTTGGGGATATGCTGCTGG 453
DB 164 ---CGAAGAAAGAGGGGCGACTCAGCATTCGGGGCTTGAGAGATCTGCTGCTCG 220
QY 454 AAGTA 459
AUTHORS 1 1 1 1
TITLE 221 AAGAA 226
JOURNAL
FEATURES

RESULT 13
LOCUS HSCACNG1 720 bp DNA linear PRI 07-JAN-2000
DEFINITION Homo sapiens calcium channel gamma 4 subunit (CACNG4) gene, exon 1.
ACCESSION AF142622
VERSION AF142622.1 GI:6062998
KEYWORDS
SEGMENT 1 of 4
SOURCE
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 720)
Burgess,D.L., Davis,C.F., Gefrides,L.A. and Noebels,J.L.
TITLE Identification of three novel Ca(2+) channel gamma subunit genes
reveals molecular diversification by tandem and chromosome
duplication
JOURNAL Genome Res. 9 (12), 1204-1213 (1999)
MEDLINE 20082967
PUBMED 10613843
REFERENCE
AUTHORS 2 (bases 1 to 720)
Burgess,D.L., Caleb,D.F., Lisa,G.A. and Jeffrey,N.L.
TITLE Direct Submission
JOURNAL Submitted (12-APR-1999) Neurology, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
FEATURES
source 1..720
location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="17"
/map="17q22-q24"
<235..454
/gene="CACNG4"
/number=1
BASE COUNT 106 a 299 c 244 g 71 t
ORIGIN
Query Match 13.2%; Score 86.4; DB 9; Length 720;
Best Local Similarity 66.8%; Pred. No. 1.1e-09;
Matches 123; Conservative 0; Mismatches 61; Indels 0; Gaps 0;
QY 214 TGTGGTGAAGAAAGGGCGTTGAGTACTGACCAACCATGGCGGCTTGGGGCTTTG 273
DB 239 TCGATGCGACCGGCGGCTGAGATGCTGTACCAAGGCGGAGCTTGGCGGCTTCT 298
QY 274 GCGTCATGACATCGCATCAGCACTGATGAGTACTGCTTACACAAGAGCTTCATCTGCA 333
DB 299 GCGTCATGCGCATTCGCGCATCGGACCGACTACTGGCTGTACTCAGCGGCACATCTGCA 358
QY 334 ACACCAACCACTCAGCAGCAGTATGACGACACACCCCATGCTGGGGGCACTGCTCT 393
DB 359 ACGGACCAACATGACATGACGACAGGGGCCCGCCCGCGCGCGCGGCGGCACTCA 418
QY 394 CCGA 397
DB 419 CCGA 422
RESULT 14
LOCUS AR165149 984 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 1 from patent US 6274380.
ACCESSION AR165149
VERSION AR165149.1 GI:16238585
KEYWORDS
SOURCE
ORGANISM Unknown.
Unclassified.
REFERENCE
AUTHORS 1 (bases 1 to 984)
Duckworth,D., Malcolm, and Hayes,P. David.
TITLE Ccanglike3 polynucleotides and expression systems
JOURNAL Patent: US 6274380-A 1 14-AUG-2001;
Location/Qualifiers

[illegible]

| | | | |
|----|-----|--|-----|
| Db | 125 | ACGGCACCACCTGACCATGTGACGACGGGGCCCCCGCCCGCGCGACCTCA | 184 |
| Qy | 394 | CCGA | 397 |
| Db | 185 | CCCA | 188 |

Search completed: February 9, 2003, 19:41:17
Job time : 2927 secs

PA (SMIK) SMITHKLINE BEECHAM PLC.

XX Duckworth DM, Hayes PD;
PI
XX
XX WPI: 2000-256976/22.
DR P-PSDB: AAY84372.
XX
XX
XX Isolated voltage-gated calcium channel polypeptide, designated
PI CACNGLIKE3, to treat diseases such as neurological disorders, epilepsy,
PI neurodegenerative disorders, cognitive disorders and cancer; comprises
PI 327 amino acid sequence -
XX
XX
PS Claim 4: Page 31: 37pp; English.
XX
XX The present sequence encodes a human skeletal muscle voltage-gated
CC calcium channel polypeptide, designated CACNGLIKE3. The CACNGLIKE3
CC polypeptide and polynucleotide are useful in the treatment of diseases
CC such as neurological disorders, epilepsy, stroke, head trauma, migraine,
CC affective disorders including depression and anxiety, schizophrenia,
CC neurodegenerative disorders including Alzheimer's disease, cognitive
CC disorders, types of pain and cancer. The polynucleotide is also valuable
CC for chromosome localisation studies. The CACNGLIKE3 polypeptide and
CC polynucleotide are also useful in diagnostic assays for detecting
CC diseases associated with inappropriate CACNGLIKE3 activity or levels.
XX
XX
SQ Sequence 984 BP; 206 A; 319 C; 265 G; 194 T; 0 other;
Query Match 13.2%; Score 86.4; DB 21; Length 984;
Best Local Similarity 66.8%; Pred. No. 1e-12;
Matches 123; Conservative 0; Mismatches 61; Indels 0; Gaps 0;
QY 214 TGTGTTGTAAGGCGCTTCAGTACTGACCAACCTGGCGCTTCGGCGCTTTG 273
DB 5 TCGGATGGCAGCGCGGCTGAGTGTGCTGACCAAGCGGAGCTTCGGCGCTTCT 64
QY 274 GCGTATGACATCGGCATGACGACGACTGCTGTACACAAAGCTCATCTGCA 333
DB 65 CGCTATGGCCATCGGCATGCGCAGCAGCTACTGCTGTACTCCAGCGGCACATCTGCA 124
QY 334 ACAGCAGCAACCTCAGCAGGAGTGATGACGACCAACCCCATGCTGGGGGAGTGGCTCT 393
DB 125 ACGGACCACTGACATGACGAGGCGGCCCGCGCGCGCGCGGCGACCTCA 184
QY 394 CCGA 397
DB 185 CCGA 188
RESULT 2
AAFB1301
ID AAFB1301 standard; cDNA; 984 BP.
XX
XX AAFB1301;
AC
XX
XX 01-JUN-2001 (first entry)
DT
XX
XX Human cacng8 cDNA.
DE
XX
XX Human; stargazin-like; CACNG8; anticonvulsant; hypotensive; vasotropic;
KW antiarhythmic; antilanginal; analgesic; nootropic; cyostatic;
KW neuroprotective; cerebroprotective; antidiabetic; antidiarrheal;
KW antiatherosclerotic; immunosuppressive; antiparkinsonian; auditory;
KW ophthalmological; tranquiliser; neuronal disorder;
KW calcium channel modulation; ss.
XX
XX
OS Homo sapiens.
XX
XX
PN WO200121791-A2.
XX
XX 29-MAR-2001.
PD
XX
XX 25-SEP-2000; 2000MO-GB03685.
PF
XX
XX 23-SEP-1999; 99GB-0022571.
PR

XX (GLAXO) GLAXO GROUP LTD.
PA
XX
XX
XX Clare JJ, Plumpton M, Moss FJ, Sansau P;
PI
XX
XX WPI: 2001-266074/27.
DR P-PSDB: AAB73979.
XX
XX
XX Novel stargazin-like polypeptides capable of modulating the steady
PI state inactivation of an alpha1 pore-forming subunit of a voltage-gated
PI calcium channel, for treating central nervous system disorders -
XX
XX
PS Claim 6: Page 38-39; 48pp; English.
XX
XX The present sequence is provided in a specification relating to an
CC isolated stargazin-like polypeptide comprising a sequence of 327 or 275
CC amino acids fully defined in the specification, or its variant capable
CC of modulating the steady state. The polypeptide is useful for treating
CC a subject having a neuronal disorder that is responsive to calcium
CC channel modulation. It is useful in the manufacture of a medicament for
CC treatment or prophylaxis of a disorder that is responsive to calcium
CC channel modulation, e.g. epilepsy, episodic ataxia, spinocerebellar
CC ataxia, hypertension, ischaemic heart disease, arrhythmia, angina,
CC pain, cerebral ischaemia, Alzheimer's disease, neuroprotection, stroke,
CC diabetes, cerebral vasospasm, atherosclerosis, tardive dyskinesias,
CC peripheral vascular disease, immunosuppression, cancerous diseases,
CC migraine, headache, bipolar disorder, unipolar depression, anxiety,
CC Parkinson's disease, cognitive disorders, ophthalmic diseases,
CC neuromuscular disorders and tinnitus. Nucleic acids encoding these
CC polypeptides are useful in the production of the polypeptides, and as
CC primers.
XX
XX
SQ Sequence 984 BP; 204 A; 319 C; 265 G; 194 T; 2 other;
Query Match 13.2%; Score 86.4; DB 22; Length 984;
Best Local Similarity 66.8%; Pred. No. 1e-12;
Matches 123; Conservative 0; Mismatches 61; Indels 0; Gaps 0;
QY 214 TGTGTTGTAAGGCGCTTCAGTACTGACCAACCTGGCGCTTCGGCGCTTTG 273
DB 5 TCGGATGGCAGCGCGGCTGAGTGTGCTGACCAAGCGGAGCTTCGGCGCTTCT 64
QY 274 GCGTATGACATCGGCATGACGACGACTGCTGTACACAAAGCTCATCTGCA 333
DB 65 CGCTATGGCCATCGGCATGCGCAGCAGCTACTGCTGTACTCCAGCGGCACATCTGCA 124
QY 334 ACAGCAGCAACCTCAGCAGGAGTGATGACGACCAACCCCATGCTGGGGGAGTGGCTCT 393
DB 125 ACGGACCACTGACATGACGAGGCGGCCCGCGCGCGCGGCGACCTCA 184
QY 394 CCGA 397
DB 185 CCGA 188
RESULT 3
ABK51915
ID ABK51915 standard; cDNA; 1071 BP.
XX
XX ABK51915;
AC
XX
XX 13-AUG-2002 (first entry)
DT
XX
XX cDNA encoding mouse Cacng4.
DE
XX
XX Mouse; neuronal voltage-gated calcium channel gamma subunit;
KW autoimmune disease; Lambert-Eaton syndrome; neuronal disease;
KW epilepsy; immunosuppressive; anticonvulsant; Cacng4; gene; ss.
XX
XX
OS Murinae gen. sp.
XX
XX
FH key Location/Qualifiers
FT 5'UTR 1..21

| | | |
|--------|---|--|
| FT | | /tag= a |
| FT | CDS | 22..1005 |
| FT | | /*tag= b |
| FT | | /product= "Cacng4 #1" |
| FT | CDS | 22..1005 |
| FT | | /*tag= c |
| FT | | /product= "Cacng4 #2 |
| FT | | /transl_except= (pos:979..981, aa:Xaa) |
| FT | | /transl_except= (pos:991..993, aa:Xaa) |
| FT | | /note= "Xaa= unknown" |
| FT | 3' UTR | 1006..1071 |
| FT | | /*tag= d |
| XX | | |
| PB | US6365337-B1. | |
| XX | | |
| PD | 02-APR-2002. | |
| XX | | |
| PE | 27-JUL-1998; | 98US-0123030. |
| PR | 27-JUL-1998; | 98US-0123030. |
| XX | | |
| PA | (IOWA) UNITV IOWA RES FOUND. | |
| XX | (JACK-) JACKSON LAB. | |
| PL | Letts VA, Frankel WN, Campbell KP, Felix R, Biddlecome G; | |
| DR | WPI: 2002-433421/46. | |
| XX | | |
| PT | P-PSDB; AAU97155, AAU97156. | |
| XX | | |
| PT | Novel nucleic acid sequences encoding a neuronal voltage-gated calcium channel gamma subunit useful in screening for compounds which modulate activity of the channel and in diagnosing, treating neuronal diseases | |
| PT | - | |
| XX | | |
| PS | Disclosure: Fig 7: 36pp: English. | |
| XX | | |
| CC | The present invention relates to the isolation of mouse genes encoding neuronal voltage-gated calcium channel gamma subunits designated Cacng2, Cacng3, and Cacng4. The genes are useful for identifying candidate compounds for modulating the activity of human neuronal voltage-gated calcium channels. They are also useful for diagnosing and treating the autoimmune disease Lambert-Eaton syndrome, as well as diagnosing defects in gamma subunit genes of a patient with a neuronal disease such as epilepsy. The present sequence encodes mouse Cacng4. | |
| CC | Note: Nucleotides 1-21 of the present sequence are not shown in Fig 7 but are included in the sequence shown in the sequence listing. | |
| CC | | |
| XX | | |
| SQ | Sequence 1071 BP: 227 A; 345 C; 284 G; 213 T; 2 other: | |
| | Query Match | 12.7%; Score 83.2; DB 24; Length 1071; |
| | Best Local Similarity | 65.8%; Pred. No. 7.le-12; |
| | Matches 121: Conservative | 0; Mismatches 63; Indels 0; Gaps 0; |
| OY | 214 TGTGCTGGAAGAAGCGCTTCAGTACTGACATGCACCATCGCGCGCTTTGG | 273 |
| Db | 26 TGCATATGGGACCGGGGCTGCAGATGCTTGCTGACCAAGGCCGAGCCCTTCT | 85 |
| OY | 274 GCCTCATGACCATTCGCATCAGCACACTGACTTGGCTCTACACAAGAGCTTCATCTGCA | 333 |
| Db | 86 CGCTCATGGCGCATTCGCATTCGGCAGCAGCATACCGGCTGATTCGAGCGGCACATCTGCA | 145 |
| OY | 334 ACACCAACCAACTCAGCAGCAGTAGTATGACGGACACACCCCATGTGTGGGGCAAGTGGCTCT | 393 |
| Db | 146 ACGGCAACCAACTGACATGACAGCAGCGGGCCCCCCCCCGCGCGCTCGCGGACCTCA | 205 |
| OY | 394 CCGA 397 | |
| Db | 206 CCGA 209 | |
| RESULT | 4 | |

| | |
|---------------------------|---|
| ABQ17108/C | ABQ17108 standard; DNA; 1093 BP. |
| ID | ABQ17108 standard; DNA; 1093 BP. |
| XX | |
| AC | ABQ17108; |
| XX | |
| DT | 12-JUL-2002 (first entry) |
| XX | |
| DE | Oligonucleotide for detecting cytosine methylation SEQ ID NO 3699. |
| XX | |
| KW | Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; |
| KW | drug; side effect; cancer; central nervous system; cardiovascular; |
| KW | gastrointestinal; respiratory system; single nucleotide polymorphism; |
| KW | SNP; cell differentiation; ds. |
| XX | |
| OS | Homo sapiens. |
| XX | |
| PN | WO200218632-A2. |
| XX | |
| PD | 07-MAR-2002. |
| XX | |
| PF | 01-SEP-2001; 2001WO-EP10074. |
| XX | |
| PR | 01-SEP-2000; 2000DE-1043826. |
| XX | |
| PR | 05-SEP-2000; 2000DE-1044543. |
| XX | |
| PA | (EPIC-) EPIGENOMICS AG. |
| XX | |
| PI | Olek A, Plepenbrock C, Berlin K, Guelig D; |
| XX | |
| DR | WPI: 2002-371829/40. |
| XX | |
| PT | Determining the degree of cytosine methylation in genomic DNA, useful |
| XX | |
| PT | for diagnosis and prognosis, comprises selective hybridization of |
| XX | |
| PT | amplicons from chemically treated DNA - |
| XX | |
| PS | Claim 12; 56bp + Sequence Listing; 56bp; German. |
| XX | |
| CC | This invention describes a novel method for determining the degree of |
| CC | methylation of a particular cytosine in a motif 5'-CpG-3', present in a |
| CC | genomic sample of DNA. The sample is treated chemically to convert |
| CC | cytosine (C) but not methylated C, to uracil, then part of the genomic |
| CC | DNA that contains the target C is amplified to form a labeled amplicon. |
| CC | The amplicon is hybridised to two classes, each with at least one |
| CC | member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers |
| CC | and the degree of hybridisation to both classes is determined from the |
| CC | label on the amplicon. From the ratio of labels hybridised to the two |
| CC | classes of oligomers, the degree of methylation is calculated. The method |
| CC | is used: (i) for diagnosis and/or prognosis of side effects of |
| CC | therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders |
| CC | of the central nervous, cardiovascular, gastrointestinal and respiratory |
| CC | systems etc., particularly by detecting mutations or single nucleotide |
| CC | polymorphisms (SNP's), and (ii) for differentiation of cell or tissue |
| CC | types and for investigating cell differentiation. The method allows the |
| CC | methylation status of many C residues to be determined simultaneously. |
| CC | ABQ13410-ABQ051121 represent genomic DNA sequences used to illustrate the |
| CC | method for determining the degree of cytosine methylation described in |
| CC | the disclosure of the invention. |
| XX | |
| SQ | Sequence 1093 BP; 95 A; 153 C; 406 G; 439 T; 0 other: |
| XX | |
| Query Match | 11.2%; Score 73.2; DB 24; Length 1093; |
| Best Local Similarity | 65.1%; Pred. No. 2.9e-09; |
| Matches 108; Conservative | 0; Mismatches 56; Indels 0; Gaps 0; |
| OY | 232 TTCAGTACTACTGACACACATCGGCGCTTCGGCGCTTTTGCCATGACCATCGCA 291 |
| DB | 683 TACAATATCTACTAACACACGACGCAACCTTCGCGCTTCGCTCATTAACCATCGCA 624 |
| OY | 292 TCAGACAGTACGACGCTCTACACAAGAGCTCATCTGCAACAACCAACCATCGCAG 351 |
| DB | 623 TCGACACGACGACTACTACTCTCAACGCGCCACATCTACAGACACCAACCTTAACCA 564 |
| OY | 352 CAGGTGATGACGACCAACCCATCGTGGGGGCGAGTGGCTCTCGCA 397 |

Db 563 TAAACGACGACCCCGCCGCCGCCGCGACGACCTCACCA 518

RESULT 5
ABQ17109
ID ABQ17109 standard; DNA; 1093 BP.

AC ABQ17109;

DT 12-JUL-2002 (first entry)

DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 3700.

Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
SNP; cell differentiation; ds.

OS Homo sapiens.

PN WO200218632-A2.

PD 07-MAR-2002.

PF 01-SEP-2001; 2001WO-EP10074.

PR 01-SEP-2000; 2000DE-1043826.

PR 05-SEP-2000; 2000DE-1044543.

PA (EPIC-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K, Guetig D;

DR WPI; 2002-371829/40.

PT Determining the degree of cytosine methylation in genomic DNA, useful
for diagnosis and prognosis, comprises selective hybridization of
amplicons from chemically treated DNA -
PS Claim 12; 56pp + Sequence Listing; 56pp; German.

CC This invention describes a novel method for determining the degree of
methylation of a particular cytosine in a motif 5'-CpG-3', present in a
genomic sample of DNA. The sample is treated chemically to convert
cytosine (C) but not methylated C, to uracil, then part of the genomic
DNA that contains the target C is amplified to form a labeled amplicon.
The amplicon is hybridised to two classes, each with at least one
member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
and the degree of hybridisation to both classes is determined from the
label on the amplicon. From the ratio of labels hybridised to the two
classes of oligomers, the degree of methylation is calculated. The method
is used: (i) for diagnosis and/or prognosis of side effects of
therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
of the central nervous, cardiovascular, gastrointestinal and respiratory
systems etc., particularly by detecting mutations or single nucleotide
polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
types and for investigating cell differentiation. The method allows the
methylation status of many C residues to be determined simultaneously.
ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the
method for determining the degree of cytosine methylation described in
the disclosure of the invention.

CC Sequence 1093 BP; 439 A; 406 C; 153 G; 95 T; 0 other;

Query Match 11.2%; Score 73.2; DB 24; Length 1093;

Best Local Similarity 65.1%; Pred. No. 2.9e-09;

Matches 108; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 232 TTCAGTACTACGACACCATCGCGCCCTTTCGGCTTTGGCCATGACATGCGCA 291
DB 411 TACAATACTACTACCGACGCAAAACCTTCCGCCCTTTCGCTATACCATCGCA 470

QY 292 TCAGCACTGACTACTGCTCTACACAGAGCTCTCATCTGCAACACCACTCAGAG 351
DB 471 TCGACACCGACTACTACTATCCACGCGCATCTTACACGACCAACCTTAACCA 530

QY 352 CAGGTGATGACGAGCACCCCATCGTGGGGGAGTGATGCTCTCCGA 397

DB 531 TAAACGACGACCCCGCCGCCGCCGCGACGACCTCACCA 576

RESULT 6
AA299795
ID AA299795 standard; DNA; 972 BP.

AC AA299795;

DT 12-JUL-2000 (first entry)

DE DNA encoding a voltage-gated calcium channel designated CACNGLIKE1.

Human; voltage-gated calcium channel; CACNGLIKE1; neurological disorder;
epilepsy; stroke; head trauma; migraine; affective disorder; depression;
anxiety; schizophrenia; neurodegenerative disorder; Alzheimer's disease;
cognitive disorder; pain; cancer; chromosome localization; ss.

OS Homo sapiens.

PN WO200014223-A1.

PD 16-MAR-2000.

PF 06-SEP-1999; 99WO-GB02937.

PR 07-SEP-1998; 98GB-0019474.

PA (SMIK) SMITHKLINE BEECHAM PLC.

PI Duckworth DM, Hayes PD;

DR WPI; 2000-256975/22.

DR P-PSDB; AAY84376.

PT New human voltage-gated calcium channel, known as CACNGLIKE1, useful in
the treatment of diseases such as neurological disorders, epilepsy,
neurodegenerative disorders, cognitive disorders and cancer, comprises
a 323 amino acid sequence -
PS Claim 4; Page 30; 35pp; English.

CC The present sequence encodes a human voltage-gated calcium channel,
known as CACNGLIKE1. The CACNGLIKE1 polypeptide and polynucleotide are
useful in the treatment of diseases such as neurological disorders,
epilepsy, stroke, head trauma, migraine, affective disorders including
depression and anxiety, schizophrenia, neurodegenerative disorders
including Alzheimer's disease, cognitive disorders, types of pain and
cancer. The polynucleotide is also valuable for chromosome localization
studies. CACNGLIKE1 polypeptide and polynucleotide are also useful in
CC diagnostic assays for detecting diseases associated with inappropriate
CACNGLIKE1 activity or levels.

CC Sequence 972 BP; 231 A; 311 C; 231 G; 199 T; 0 other;

Query Match 8.3%; Score 54.4; DB 21; Length 972;

Best Local Similarity 70.2%; Pred. No. 0.00022;

Matches 73; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 218 GTGTGAAAAGGCGCTTACGACTACTGACACCATCGCGCCTTTCGGGCTTTGGCCT 277
DB 9 GTTGTATGAGGTGTCAATGCTTTTAACACCGCTTGGTGGCTGCTGCCTTCAAGCT 68

PR 12-NOV-1998; 98US-0191283.
PR 09-DEC-1998; 98US-0208821.
PR 26-JAN-1999; 99US-0237506.
PR 10-FEB-1999; 99US-0247891.
XX
XX
PA (INCYTE) INCYTE PHARM INC.
XX
XX Au-Young J, Bandman O, Tang YT, Reddy R, Hillman JL, Yue H;
PI Lai P, Corley NC, Guegler KJ, Gorgone G, Baughn MR, Azimzal Y;
XX
DR WPI: 2000-256643/22.
P-PSDB: AAU70462.
XX
XX Novel human membrane channel protein and polynucleotide useful for
PT diagnosing and treating cell proliferative, inflammatory, secretory,
PT osmoregulatory, muscular, cardiovascular and neurological disorders
XX
XX
PS Claim 9; Page 126; 140pp; English.
XX
XX The present sequence is a cDNA identified in Incyte clone 1267774
CC derived from BRAINOT09 cDNA library. It encodes human membrane channel
CC protein-12 (MECHP-12), which is expressed in nervous tissues. Anti-MECHP
CC antibodies can be used as therapeutic antagonists and reagents for
CC diagnosis and monitoring diseases. MECHP cDNA can be used for diagnosis
CC of MECHP-related diseases and gene mapping. MECHP can be used for
CC treatment of cell proliferative disorders such as bursitis and
CC atherosclerosis, cancers like lymphoma and sarcoma, inflammatory
CC disorders like AIDS and Addison's disease, transport/secretory disorders
CC like cystic fibrosis and diabetes mellitus, osmoregulatory disorders like
CC diarrhea and renal failure, muscular disorders like myocarditis and
CC Duchenne's muscular dystrophy, cardiovascular disorders like hypertension
CC and vasculitis, congenital lung anomalies like bronchitis and asthma and
CC neurological diseases like Alzheimer's disease, Parkinson's disease and
CC Huntington's disease.
XX
SQ Sequence 1478 BP; 374 A; 416 C; 339 G; 349 T; 0 other;

Query Match 8.3%; Score 54.4; DB 21; Length 1478;
Best Local Similarity 70.2%; Pred. No. 0.00025;
Matches 73; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

OY 218 GGTGTGAAAAGGCGCTTCAGTACTACTGACACATCGGCGCTTGGCGCTTTGGCCT 277
DB 372 GTTTGATCGAGGTTTCAATATGCTTTTACACACCGTTGTGCTTGCCTTCAGCCT 431
OY 278 CATGACCATCGCATCAGCAGTACTGCTCTACACAGAAG 321
DB 432 GATGACCATGAGCTGTGGGAACGACATATTGGCTTACTCTCAGAG 475

RESULT 9
ABK51914
ID ABK51914 standard: cDNA; 1477 BP.
XX
XX ABK51914;
XX
XX 13-AUG-2002 (first entry)
XX
XX cDNA encoding mouse Cacng3.
XX
XX
XX Mouse; neuronal voltage-gated calcium channel gamma subunit;
KM autoimmune disease; Lambert-Eaton syndrome; neuronal disease;
KW epilepsy; immunosuppressive; anticonvulsant; Cacng3; gene; ss.
XX
XX
OS Murinae gen. sp.
XX
XX
FH Key Location/Qualifiers
FT 5'UTR 1..487
FT CDS 488..1435
FT FT /*tag= a
FT FT /*tag= b
FT FT /product= "Cacng3"
FT 3'UTR 1436..1477

FT /*tag= C
XX US6365337-B1.
PN 02-APR-2002.
XX
XX 27-JUL-1998; 98US-0123030.
XX
XX
XX 27-JUL-1998; 98US-0123030.
PR 27-JUL-1998; 98US-0123030.
XX
XX
XX (IOWA) UNIV IOWA RES FOUND.
PA (JACK-) JACKSON LAB.
XX
XX
XX Letts VA, Frankel WN, Campbell KP, Felix R, Biddlecome G;
PI WPI: 2002-433421/46.
DR P-PSDB: AAU97154.
XX
XX Novel nucleic acid sequences encoding a neuronal voltage-gated calcium
PT channel gamma subunit useful in screening for compounds which modulate
PT activity of the channel and in diagnosing, treating neuronal diseases
XX
XX
PS Disclosure: Fig 6; 36pp; English.
XX
XX The present invention relates to the isolation of mouse genes
CC encoding neuronal voltage-gated calcium channel gamma subunits
CC designated Cacng2, Cacng3, and Cacng4. The genes are useful for
CC identifying candidate compounds for modulating the activity of human
CC neuronal voltage-gated calcium channels. They are also useful for
CC diagnosing and treating the autoimmune disease Lambert-Eaton
CC syndrome, as well as diagnosing defects in gamma subunit genes of a
CC patient with a neuronal disease such as epilepsy. The present
CC sequence encodes mouse Cacng3.
XX
SQ Sequence 1477 BP; 352 A; 449 C; 356 G; 320 T; 0 other;

Query Match 8.2%; Score 53.6; DB 24; Length 1477;
Best Local Similarity 66.4%; Pred. No. 0.0004;
Matches 77; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

OY 218 GGTGTGAAAAGGCGCTTCAGTACTACTGACACATCGGCGCTTGGCGCTTTGGCCT 277
DB 496 GTGTGACAGAGATTCACATATGTTGATCCTGTAGGAGCCTTCGACGTTTAGTTT 555
OY 278 CATGACCATCGCATCAGCAGTACTGCTCTACACAGAAGCTCTATCTGCA 333
DB 556 AATGACCATTCAGTGTGGCAGCAGACTACTGCTATATTCCAGAGGTGTGCAGGA 611

RESULT 10
ABK51913
ID ABK51913 standard: cDNA; 1558 BP.
XX
XX ABK51913;
XX
XX 13-AUG-2002 (first entry)
XX
XX cDNA encoding mouse Cacng2.
XX
XX
XX Mouse; neuronal voltage-gated calcium channel gamma subunit;
KM autoimmune disease; Lambert-Eaton syndrome; neuronal disease;
KW epilepsy; immunosuppressive; anticonvulsant; Cacng2; gene; ss.
XX
XX
OS Murinae gen. sp.
XX
XX
FH Key Location/Qualifiers
FT 5'UTR 1..389
FT CDS 390..1361
FT FT /*tag= a
FT FT /*tag= b
FT FT /product= "Cacng2"
FT 3'UTR 1362..1558

```

FT XX /*tag= c
PN XX US6365337-B1.
PD XX 02-APR-2002.
PF XX 27-JUL-1998; 98US-0123030.
PR XX 27-JUL-1998; 98US-0123030.
XX XX
XX (IOWA ) UNIV IOWA RES FOUND.
XX (JACK-) JACKSON LAB.
XX
XX Lects VA, Frankel WN, Campbell KP, Felix R, Biddlecome G;
XX
XX WPI: 2002-433421/46.
XX P-PSDB: AAU97153.
XX
XX Novel nucleic acid sequences encoding a neuronal voltage-gated calcium
XX channel gamma subunit useful in screening for compounds which modulate
XX activity of the channel and in diagnosing, treating neuronal diseases
XX
XX Claim 2: Fig 2: 36pp; English.
XX
XX The present invention relates to the isolation of mouse genes
XX encoding neuronal voltage-gated calcium channel gamma subunits
XX designated Cacng2, Cacng3, and Cacng4. The genes are useful for
XX identifying candidate compounds for modulating the activity of human
XX neuronal voltage-gated calcium channels. They are also useful for
XX diagnosing and treating the autoimmune disease Lambert-Eaton
XX syndrome, as well as diagnosing defects in gamma subunit genes of a
XX patient with a neuronal disease such as epilepsy. The present
XX sequence encodes mouse Cacng2.
XX
XX Sequence 1558 BP; 418 A; 441 C; 360 G; 339 T; 0 other;
XX
XX Query Match 8.0%; Score 52.8; DB 24; Length 1558;
XX Best Local Similarity 69.2%; Pred. No. 0.00066;
XX Matches 72; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
XX
XX 218 GTGTGAAGAAGGCGCTTCAGTACTGACCATCGGCGCTTCGCGCTTTGGCCT 277
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX Db 398 GTTTGATGAGAGGTTCATGATGCTTTTACACCGCTTGCCTTCAGCTT 457
XX
XX 278 CATGACCATCGCCATGACACTGACTGCTCTACACAAGAG 321
XX ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX Db 458 GATGACCATCGCTGTGGAACGACGACTATTGGCTACTCCAGAG 501
XX
XX RESULT 11
XX AA299794
XX ID AA299794 standard; DNA: 945 BP.
XX
XX AA299794:
XX
XX 12-JUL-2000 (first entry)
XX
XX EST corresponding to a neuronal voltage-gated calcium channel DNA.
XX
XX Human: neuronal voltage-gated calcium channel: gamma-2 subunit;
XX gamma-3 subunit; CACNGLIKE2; neurological disorder; epilepsy; stroke;
XX head trauma; migraine; affective disorder; depression; anxiety;
XX schizophrenia; neurodegenerative disorder; Alzheimer's disease;
XX cognitive disorder; pain; cancer; vaccine; expressed sequence tag;
XX EST; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..945
XX FT /*tag= a
XX

```

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PN XX WO200014225-A1.
XX
XX 16-MAR-2000.
XX
XX 06-SEP-1999; 99WO-GB02945.
XX
XX 08-SEP-1998; 98GB-0019589.
XX
XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX Duckworth DM, Hayes PD;
XX
XX WPI: 2000-256977/22.
XX P-PSDB: AAY84375.
XX
XX CACNGLIKE polynucleotides and polypeptides, useful in diagnostic assays
XX and for treating conditions such as Alzheimer's -
XX
XX Claim 11: Page 31; 33pp; English.
XX
XX The present sequence represents an expressed sequence tag (EST)
XX corresponding to a putative human neuronal voltage-gated calcium
XX channel gamma-2 and gamma-3 subunits, designated CACNGLIKE2
XX polypeptides. The CACNGLIKE2 polynucleotide and polypeptide are
XX useful for treating neurological disorders, epilepsies, stroke, head
XX trauma, migraine, affective disorders including depression and anxiety,
XX schizophrenia, neurodegenerative disorders including Alzheimer's disease,
XX cognitive disorders, pain and cancer. They may also be used to configure
XX screening methods for detecting the effect of added compounds on the
XX production of mRNA in cells. The polypeptides may also be used as
XX vaccines to induce an immunological response in mammals.
XX
XX Sequence 945 BP; 232 A; 274 C; 217 G; 222 T; 0 other;
XX
XX Query Match 7.9%; Score 52; DB 21; Length 945;
XX Best Local Similarity 65.5%; Pred. No. 0.00091;
XX Matches 76; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
XX
XX 218 GTGTGAAGAAGGCGCTTCAGTACTGACCATCGGCGCTTCGCGCTTTGGCCT 277
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX Db 9 GTGTGACAGAGGTATCCGATGTGATCACCATGCTAGACCTTTGGCTTTAGTTT 68
XX
XX 278 CATGACCATCGCCATGACACTGACTGCTCTACACAAGAGTCTCATCTGCA 333
XX ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX Db 69 AATGACCATTCGACGTGGCAGGACTGCTTATATTCAGAGGTGTGCAGGA 124
XX
XX RESULT 12
XX AA299793
XX ID AA299793 standard; DNA: 948 BP.
XX
XX AA299793:
XX
XX 12-JUL-2000 (first entry)
XX
XX DNA encoding a neuronal voltage-gated calcium channel.
XX
XX Human: neuronal voltage-gated calcium channel: gamma-2 subunit;
XX gamma-3 subunit; CACNGLIKE2; neurological disorder; epilepsy; stroke;
XX head trauma; migraine; affective disorder; depression; anxiety;
XX schizophrenia; neurodegenerative disorder; Alzheimer's disease;
XX cognitive disorder; pain; cancer; vaccine; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..948
XX FT /*tag= a
XX FT /product= "voltage-gated calcium channel"
XX
XX WO200014225-A1.
XX
XX 16-MAR-2000.
XX

```

XX 06-SEP-1999; 99WO-GB02945.
 PF 08-SEP-1998; 98GB-0019589.
 XX (SMIK) SMITHKLINE BEECHAM PLC.
 PA Duckworth DM, Hayes PD;
 PI WPI: 2000-256977/22.
 DR P-PSDB: AAY84374.
 XX
 PT CACNGLIKE polynucleotides and polypeptides, useful in diagnostic assays
 PT and for treating conditions such as Alzheimer's -
 PS
 PS Claim 4: Page 29; 33pp; English.
 CC The present sequence encodes a putative human neuronal voltage-gated
 CC calcium channel gamma-2 and gamma-3 subunits, designated CACNGLIKE2
 CC polypeptides. The CACNGLIKE2 polynucleotide and polypeptide are
 CC useful for treating neurological disorders, epilepsies, stroke, head
 CC trauma, migraine, affective disorders including depression and anxiety,
 CC schizophrenia, neurodegenerative disorders including Alzheimer's disease,
 CC cognitive disorders, pain and cancer. They may also be used to configure
 CC screening methods for detecting the effect of added compounds on the
 CC production of mRNA in cells. The polypeptides may also be used as
 CC vaccines to induce an immunological response in mammals.
 XX
 XX Sequence 948 BP; 234 A; 273 C; 218 G; 223 T; 0 other;
 Query Match 7.9%; Score 52; DB 21; Length 948;
 Best Local Similarity 65.5%; Pred. No. 0.00091;
 Matches 76; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
 OY 218 GGTGTGAAAAGGCGTTCAGTACTGACACGACGCGGCGCTTTGGCCT 277
 DB 9 GTGTGACAGAGGTATCCAGATGTGATCCACACTGTAGAGACCTTTGCCGCTTTAGTTT 68
 OY 278 CATGACCATGGCATCAGCATGACTGCTGTACACAGAGCTCTCATCTGCA 333
 DB 69 AATGACCATTTGACGTGGCAGCGAGCTACTGTTATTTCCAGAGGTGTGACAGGA 124
 RESULT 13
 ABA09004 standard; CDNA: 1383 BP.
 AC ABA09004;
 XX 11-JAN-2002 (first entry)
 DE Human voltage gated Cl channel subunit homologue cDNA, SEQ ID NO:780.
 XX
 KM Human: cytokine; cell proliferation; tissue growth; immunomodulator; growth factor;
 KM haematopoiesis regulation; tissue growth; immunomodulator; growth factor;
 KM inhibin; chemokinesis; chemokinesis; thrombolytic; oncogenesis;
 KM proliferation; metastasis; cancer; tumour; haematopoietic disorder;
 KM myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
 KM chronic inflammatory condition; proliferative retinopathy;
 KM atherosclerosis; coronary heart disease; arterial ischaemia;
 KM bone disorder; osteoporosis; vascular growth disorder;
 KM tissue regeneration; wound healing; infection; immune disorder;
 KM cell culture; drug screening; gene therapy; antiinflammatory;
 KM antiasthmatic; antiarthritis; haemostatic; antiarteriosclerotic;
 KM cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
 KM antifungal; vulnery; antitumor; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200157188-A2.
 XX
 PD 09-AUG-2001.
 XX

PF 05-FEB-2001; 2001WO-US03800.
 XX 03-FEB-2000; 2000US-0496914.
 PR 27-APR-2000; 2000US-0560875.
 XX (HYSE-) HYSEQ INC.
 PA Tang YF, Liu C, Dirmanac RT;
 PI WPI: 2001-457740/49.
 DR P-PSDB: ABB11760.
 XX
 PT Human proteins and DNA encoding sequences useful for preventing,
 PT treating or ameliorating a medical condition in a mammalian subject
 PT e.g. arthritis and cancer -
 PS
 PS Claim 1: Page 691-692; 1963pp; English.
 CC Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
 CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
 CC invention also relates to vectors and recombinant host cells comprising a
 CC nucleotide of the invention, methods of producing the novel polypeptides,
 CC antibodies against the polypeptides, methods of detecting the nucleotides
 CC or polypeptides in a sample, and methods of identifying compounds which
 CC bind to polypeptides of the invention. Although novel, many of the
 CC polypeptides of the invention have homology to known proteins, thereby
 CC giving an insight into their probable biological activities, and hence
 CC potential therapeutic applications. The polypeptides of the invention may
 CC have various activities, including cytokine, cell proliferation or cell
 CC differentiation activities; stem cell growth factor activity;
 CC haematopoiesis regulatory activity; tissue growth activity;
 CC immunomodulatory activity; activin- or inhibin-related activities;
 CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
 CC thrombolytic activities; receptor or ligand activities; or may be
 CC involved in oncogenesis, cancer cell proliferation or metastasis.
 CC Depending on their biological activities, polypeptides and nucleotides of
 CC the invention are useful for preventing, treating or ameliorating medical
 CC conditions, e.g., by protein or gene therapy. Such conditions include
 CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
 CC disorders), chronic inflammatory disorders (e.g., asthma or arthritis),
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,
 CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
 CC vascular growth. Polypeptides involved with tissue regeneration and
 CC repair (or nucleic acids encoding them) may be used to promote wound
 CC healing (e.g., of burns, incisions and ulcers), while those with
 CC immunomodulatory activities may be used in the treatment of viral,
 CC bacterial and fungal infections in addition to immune disorders.
 CC Polypeptides with growth factor activity may be used in cell cultures to
 CC promote cell growth. For example, such polypeptides may be used to
 CC manipulate stem cells in culture to give rise to neuroepithelial cells
 CC that can be used to augment or replace cells damaged by illness,
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides
 CC may also be used in the diagnosis of the above conditions, and in drug
 CC screening techniques. The present sequence represents a cDNA encoding a
 CC novel human polypeptide of the invention.
 XX
 XX Sequence 1383 BP; 336 A; 407 C; 341 G; 299 T; 0 other;
 Query Match 7.9%; Score 52; DB 22; Length 1383;
 Best Local Similarity 65.5%; Pred. No. 0.001;
 Matches 76; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
 OY 218 GGTGTGAAAAGGCGTTCAGTACTGACACGACGCGGCGCTTTGGCCT 277
 DB 429 GTGTGACAGAGTATCCAGATGTGATCCACACTGTAGAGACCTTTGCCGCTTTAGTTT 488
 OY 278 CATGACCATGGCATCAGCATGACTGCTGTACACAGAGCTCTCATCTGCA 333
 DB 489 AATGACCATTTGACGTGGCAGCGAGCTACTGTTATTTCCAGAGGTGTGACAGGA 544
 RESULT 14
 AAC77216

ID AAC77216 standard; cDNA; 1854 BP.
 XX AAC77216;
 XX 08-FEB-2001 (first entry)
 DE Human ORFX ORF2771 polynucleotide sequence SEQ ID NO:5541.
 XX
 KW Human: open reading frame; ORFX; detection: cytostatic; hepatotropic;
 KW vulnereary; antiparalytic; antiparkinsonian; neurotropic; neuroprotective;
 KW immunosuppressant; osteoporotic; antidiabetic; immunosuppressant; cardiac;
 KW immunostimulant; thrombolytic; coagulant; vasotrophic; antidiabetic;
 KW hypotensive; dermatological; immunosuppressive; antidiabetic;
 KW antiviral; antibacterial; antifungal; antirheumatic; antihypertensive;
 KW antianemic; gene therapy; cancer; proliferative disorder; hypertension;
 KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
 KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
 KW cholesterol ester storage; systemic lupus erythematosus; infection;
 KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
 KW allergy; aplastic anemia; nocturnal hemoglobinuria; burn; wound;
 KW bone damage; cartilage damage; antidiabetic disease; coagulation;
 KW thrombosis; contraceptive; ss.
 KW
 XX Homo sapiens.
 OS
 XX MO300058473-A2.
 PN
 XX 05-OCT-2000.
 PD
 XX
 XX 31-MAR-2000; 2000WO-US08621.
 PE
 XX 31-MAR-1999; 99US-0127607.
 PR 02-APR-1999; 99US-0127636.
 PR 03-APR-1999; 99US-0127728.
 PR 30-MAR-2000; 2000US-0540763.
 PR
 PA (CURA-) CURAGEN CORP.
 PI Shinkets RA, Leach M;
 DR WPI: 2000-602362/57.
 P-PSDB; AAB43007.
 XX
 PT Novel nucleic acids and peptides derived from open reading frame X.
 PT useful for treating e.g. cancers, proliferative disorders,
 PT neurodegenerative disorders and cardiovascular disease -
 PT
 XX
 PS Claim 5; Page 4724-4725; 5507pp; English.
 XX
 CC AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
 CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
 CC sequences have activities such as: cytostatic; hepatotropic; vulnereary;
 CC antiparalytic; antiparkinsonian; neurotropic; neuroprotective;
 CC osteoporotic; antidiabetic; immunosuppressant;
 CC immunostimulant; cardiac; thrombolytic; coagulant; vasotrophic;
 CC antidiabetic; hypotensive; dermatological; immunosuppressive;
 CC antidiabetic; antidiabetic; antiviral; antirheumatic; antihypertensive;
 CC antidiabetic; antidiabetic; antidiabetic; antidiabetic;
 CC the presence of or predisposition to, or preventing or treating
 CC pathological conditions associated with an ORFX-associated disorder. The
 CC nucleic acids can be used to express ORFX proteins in gene therapy.
 CC vectors. The proteins and nucleic acids may be used to treat cancers,
 CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
 CC graft vs host disease, cardiovascular disease, diabetes mellitus,
 CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
 CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
 CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
 CC allergies, aplastic anemia, burns, wounds, bone and cartilage damage,
 CC nocturnal hemoglobinuria, antidiabetic disease; to enhance
 CC coagulation; to inhibit thrombosis; and as a contraceptive.
 CC
 XX Sequence 1854 BP; 460 A; 549 C; 414 G; 429 T; 2 other;

Query Match 7.9%; Score 52; DB 21; Length 1854;
 Best Local Similarity 65.5%; Pred. No. 0.0011;
 Matches 76; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
 OY 218 GTGTGAAGGCGTTAGTACTGACGACCATCGCGCTTGGGCTTTGGCT 277
 DB 354 GTGTGACAGAGGTATTCAGATGTTGATCACCACCTGTAGAGCTTTGGCGCTTTAGTTT 413
 OY 278 CATGACCATTCGCTGACGACTGACTGCTGCTTACACAGAGCTTCATTCGA 333
 DB 414 AATGACCATTCGCTGACGAGGCGACGACTGCTGCTTATTCAGAGGTGTGTGACGA 469
 RESULT 15
 ID AAV55831/C
 AA V55831 standard; DNA; 799 BP.
 XX
 AC AAV55831;
 XX
 DT 18-NOV-1998 (first entry)
 XX
 DE Nucleotide sequence of the stabilising sequence-encoding insert.
 DE
 KW Fusion protein; stabilising polypeptide; proteolytic degradation;
 KW resistance; half-life; autoimmune disease; inflammation; nitro drug;
 KW IkappaB regulator protein; inflammatory bowel disease; in vivo imaging;
 KW nitroreductase protein; enzyme therapy; produg therapy; protease;
 KW cancer; pathological condition; ss.
 KW
 XX Epstein-barr virus.
 OS
 XX WO9822577-A1.
 PN
 XX 28-MAY-1998.
 PD
 XX 17-NOV-1997; 97WO-IB01508.
 PE
 XX 25-JUN-1997; 97US-0048945.
 PR 15-NOV-1996; 96US-0030986.
 PR
 PA (MASU/) MASUCCI M G.
 PI Masucci MG;
 DR WPI: 1998-312463/27.
 XX
 PT New fusion proteins resistant to proteolytic degradation -
 PT comprising a core protein with a stabilising polypeptide comprising
 PT a peptide sequence containing glycine repeats
 PT
 XX
 PS Disclosure: Fig 4B; 120pp; English.
 XX
 CC This is a nucleotide sequence of the stabilising sequence-encoding
 CC insert. The invention provides a method for increasing the resistance
 CC of a core protein to proteolytic degradation that comprises linking or
 CC inserting onto or into the core protein a stabilising polypeptide of
 CC formula (Gly)_nX(Gly)_mY(Gly)_pZ where Gly, Glyb, Glyc are 1-6
 CC sequential Gly residues and X, Y, Z are Ala, Ser, Val, Ile, Leu, Met,
 CC Phe, Pro or Thr and n can be anything between 1-66. X, Y and Z need not
 CC be identical from n repeat to n repeat. Alternatively a nucleic acid
 CC encoding the stabilising polypeptide can be linked onto or inserted into
 CC a nucleic acid encoding a core protein. The fusion proteins of the
 CC invention are more resistant to degradation by proteases and, thus, have
 CC a longer half-life than the unfused core protein. The products can be
 CC used for treating autoimmune diseases, cancer and inflammation. In
 CC particular, the core protein may be an IkappaB regulator protein for the
 CC treatment of inflammatory bowel disease, or a nitroreductase protein
 CC which can activate nitro drugs in enzyme/produg therapy to treat cancer
 CC or other pathological conditions. The fusion proteins can also be used in
 CC diagnostic methods such as in vivo imaging.
 CC
 XX Sequence 799 BP; 201 A; 106 C; 479 G; 13 T; 0 other;

Query Match 6.5%; Score 42.8; DB 19; Length 799;
 Best Local Similarity 58.7%; Pred. No. 0.21;
 Matches 74; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 13 CTGCACCTTCGCTCGACGACACCTGCTGCGCCGCGCCCTCTGCGCCCTTGAG 72
 DB 740 CTGCACCTTCGCTCGACGACACCTGCTGCGCCGCGCCCTCTGCGCCCTTGAG 681
 QY 73 GCGCCCGACCTTCGCTGCTGCTGATCCCGCCAGCGCGGACGCGCCGCTCGCG 132
 DB 680 CCGCTGCTGCTGCTGCGCCCTCGCGCCCGCTGCTGCGCCCTCGCGCCCTCGCTG 621
 QY 133 TGCCCG 138
 DB 620 CTGCGCC 615

Search completed: February 9, 2003, 18:52:19
 Job time : 229 secs


```
RESULT 2
US-09-765-205-43
: Sequence 43, Application US/09765205
: Patent No. US20020034800A1
: GENERAL INFORMATION:
: APPLICANT: Cao, Li
: TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES
: FILE REFERENCE: 1458.004/200130.449
: CURRENT APPLICATION NUMBER: US/09/765,205
: CURRENT FILING DATE: 2001-01-17
: PRIOR APPLICATION NUMBER: US/09/212,440
: PRIOR FILING DATE: 1998-12-16
: NUMBER OF SEQ ID NOS: 46
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 43
: LENGTH: 1152
: TYPE: DNA
: ORGANISM: human
US-09-765-205-43

Query Match          6.1%; Score 40; DB 10; Length 1152;
Best Local Similarity 53.9%; Pred. No. 0.14;
Matches 82; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

Qy 22 CGCCTCTGCAGCACCCTGCTCGTCCGCGCCGCTCTGCGCCCTTGAGGCGCCCGCAG 81
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 116 CGCCTGAGACAGCCCGCGGCGGCGCCCTCGACCTCTGCGCCGCGGCGGCGGCT 175
Qy 82 CTTCTGCGCTGCTGTGATCCCCCAGCGCGCGGCGCGCCGCTCGCTGCGCCGCT 141
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 176 CCCCTCCCGCGCGCTGTCTCCCAAGGCGGAGGCGCGGCGCTCCAGCCCGCAGCCCGCC 235
Qy 142 GGTGCGCCAGCGCCCGCGGCTGCCAGTGGTG 173
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 236 GGGGTCCCTGGGGAGCGCGCGCGCGCAGTGT 267

RESULT 3
US-09-944-413-41/c
: Sequence 41, Application US/09944413
: Patent No. US20020156004A1
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin
: APPLICANT: Botstein, David
: APPLICANT: Eaton, Dan
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Fliviaroff, Ellen
: APPLICANT: Gerltsen, Mary
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul
: APPLICANT: Grimaldi, Christopher
: APPLICANT: Gurney, Austin
: APPLICANT: Hillan, Kenneth
: APPLICANT: Kijavin, Ivar
: APPLICANT: Napier, Mary
: APPLICANT: Roy, Margaret
: APPLICANT: Tumas, Daniel
: APPLICANT: Wood, William
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P2548P1C1
: CURRENT APPLICATION NUMBER: US/09/944,413
: CURRENT FILING DATE: 2001-09-26
: PRIOR APPLICATION NUMBER: 09/866,028
: PRIOR FILING DATE: 2001-05-25
: PRIOR APPLICATION NUMBER: 60/067,411
: PRIOR FILING DATE: December 3, 1997
: PRIOR APPLICATION NUMBER: 60/069,334
: PRIOR FILING DATE: December 11, 1997
: PRIOR APPLICATION NUMBER: 60/069,335
: PRIOR FILING DATE: December 11, 1997
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: PRIOR APPLICATION NUMBER: 60/069,278
: PRIOR FILING DATE: December 11, 1997
: PRIOR APPLICATION NUMBER: 60/069,425
: PRIOR FILING DATE: December 12, 1997
: PRIOR APPLICATION NUMBER: 60/069,696
: PRIOR FILING DATE: December 16, 1997
: PRIOR APPLICATION NUMBER: 60/069,694
: PRIOR FILING DATE: December 16, 1997
: PRIOR APPLICATION NUMBER: 60/069,702
: PRIOR FILING DATE: December 16, 1997
: PRIOR APPLICATION NUMBER: 60/069,870
: PRIOR FILING DATE: December 17, 1997
: PRIOR APPLICATION NUMBER: 60/069,873
: PRIOR FILING DATE: December 17, 1997
: PRIOR APPLICATION NUMBER: 60/068,017
: PRIOR FILING DATE: December 18, 1997
: PRIOR APPLICATION NUMBER: 60/070,440
: PRIOR FILING DATE: January 5, 1998
: PRIOR APPLICATION NUMBER: 60/074,086
: PRIOR FILING DATE: February 9, 1998
: PRIOR APPLICATION NUMBER: 60/074,092
: PRIOR FILING DATE: February 9, 1998
: PRIOR APPLICATION NUMBER: 60/075,945
: PRIOR FILING DATE: February 25, 1998
: PRIOR APPLICATION NUMBER: 60/112,850
: PRIOR FILING DATE: December 16, 1998
: PRIOR APPLICATION NUMBER: 60/113,296
: PRIOR FILING DATE: December 22, 1998
: PRIOR APPLICATION NUMBER: 60/146,222
: PRIOR FILING DATE: July 28, 1999
: PRIOR APPLICATION NUMBER: PCT/US98/19330
: PRIOR FILING DATE: September 16, 1998
: PRIOR APPLICATION NUMBER: PCT/US98/25108
: PRIOR FILING DATE: December 1, 1998
: PRIOR APPLICATION NUMBER: 09/216,021
: PRIOR FILING DATE: December 16, 1998
: PRIOR APPLICATION NUMBER: 09/218,517
: PRIOR FILING DATE: December 22, 1998
: PRIOR APPLICATION NUMBER: 09/254,311
: PRIOR FILING DATE: March 3, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/12252
: PRIOR FILING DATE: June 22, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/21090
: PRIOR FILING DATE: September 15, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/28409
: PRIOR FILING DATE: No. US20020156004A1eember 30, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/28313
: PRIOR FILING DATE: No. US20020156004A1eember 30, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/28301
: PRIOR FILING DATE: December 1, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/30095
: PRIOR FILING DATE: December 16, 1999
: PRIOR APPLICATION NUMBER: PCT/US00/03565
: PRIOR FILING DATE: February 11, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/04414
: PRIOR FILING DATE: February 22, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/05841
: PRIOR FILING DATE: March 2, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/08439
: PRIOR FILING DATE: March 30, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/14042
: PRIOR FILING DATE: May 22, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/20710
: PRIOR FILING DATE: July 28, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/32678
: PRIOR FILING DATE: December 1, 2000
: PRIOR APPLICATION NUMBER: PCT/US01/06520
: PRIOR FILING DATE: February 28, 2001
: NUMBER OF SEQ ID NOS: 120
: SEQ ID NO 41
: LENGTH: 1377
: TYPE: DNA
: ORGANISM: Homo Sapien
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RESULT 5

RESULT 5

US-09-944-896-41/C
Sequence 41, Application US/09944896
Patent No. US20020168715A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Kijavlin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944, 896
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 09/866, 028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/069, 334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069, 335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069, 278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069, 425
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069, 696
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069, 694
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069, 702
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069, 870
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069, 873
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/068, 017
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/070, 440
PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/074, 086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074, 092
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075, 945
PRIOR FILING DATE: February 25, 1998
PRIOR APPLICATION NUMBER: 60/112, 850
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113, 296
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/146, 222
PRIOR FILING DATE: July 28, 1999
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: September 16, 1998
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: December 1, 1998
PRIOR APPLICATION NUMBER: 09/216, 021
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/218, 517
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254, 311
PRIOR FILING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: June 22, 1999

PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: No. US20020168715A1,ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: No. US20020168715A1,ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December 1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR FILING DATE: February 11, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 41
LENGTH: 1377
TYPE: DNA
ORGANISM: Homo Sapien
US-09-944-896-41
Query Match 6.1%; Score 39.8; DB 9; Length 1377;
Best Local Similarity 56.5%; Pred. No. 0.17;
Matches 74; Conservative 0; Mismatches 57; Indels 0; Gaps 0;
QY 37 CTGTCGCTGCCCCCGCCCTGTGAGCCCTTGAGCCGCCACCTCTGCTGCTG 96
DB 479 CTCCTCGGGGCGCCGCGGTCCTCGAGGTCGCGGAGTCGCCCTCCGCGCCCTT 420
QY 97 TGATCCCCCAGCCCGCGGAGCGCCCGCTCGCTGCGCCCGGTGTGCGCCAGGGCC 156
DB 419 TCTCTCCGAGCCCGCGGCGCGCTGCGGCGCTGCGGCGCATGCGGCGCGCAAGC 360
QY 157 CCCGGTGGCA 167
DB 359 CCTGGCTGCCA 349
RESULT 6
US-09-944-944-41/C
Sequence 41, Application US/09944944
Patent No. US20020173463A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Kijavlin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: ACIDS ENCODING THE SAME

FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944,944
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069,596
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,594
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,702
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,870
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069,873
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/068,017
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/070,440
PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/074,086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074,092
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075,945
PRIOR FILING DATE: February 25, 1998
PRIOR APPLICATION NUMBER: 60/112,850
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113,296
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/146,222
PRIOR FILING DATE: July 28, 1999
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: September 16, 1998
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: December 1, 1998
PRIOR APPLICATION NUMBER: 09/216,021
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/218,517
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254,311
PRIOR FILING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: June 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: No. US20020173463A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: No. US20020173463A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December 1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR FILING DATE: February 11, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: May 22, 2000

PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 41
LENGTH: 1377
TYPE: DNA
ORGANISM: Homo Sapien
US-09-944-944-41

Query Match 6.1%; Score 39.8; DB 9; Length 1377;
Best Local Similarity 56.5%; Pred. No. 0.17;
Matches 74; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 37 CTGCTGCTGCCCCCGGCGCCCTCTGCGCCCTTGAGCGCCCGACGCTTCTGCTGTGCTG 96
|| ||||| ||||| || ||||| || || ||||| || ||||| ||
Db 479 CTCTCGCGGCGCCGCGGCTCCCTCGAGGTCCCGGAGTCCCGGCGCTCCCGGCTCGCTT 420
QY 97 TGATCCCCCGGCGCGGCGCCCGCTCGGCTGCCCCGGTGTGCGCCAGGCGCC 156
|| ||||| ||||| || ||||| || ||||| || ||||| ||
Db 419 TCTCTCCGCGAGCCCGGCGCGCTCGCGCGCTCGCGGCGATCGCGCGCGGCGAGC 360
QY 157 CCGGTTGCCA 167
|| || |||||
Db 359 CCGGCTGCCA 349

RESULT 7

US-09-944-907-41/C
Sequence 41, Application US/09944907
Publication No. US20020198147A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Baton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary
APPLICANT: Godowsky, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Kilgavin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944,907
PRIOR FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 41
LENGTH: 1377
TYPE: DNA
ORGANISM: Homo Sapien
US-09-944-907-41

Query Match 6.1%; Score 39.8; DB 9; Length 1377;
Best Local Similarity 56.5%; Pred. No. 0.17;
Matches 74; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 37 CTGCTGCTGCCCCCGGCGCCCTCTGCGCCCTTGAGCGCCCGACGCTTCTGCTGTGCTG 96
|| ||||| ||||| || ||||| || || ||||| || ||||| ||
Db 479 CTCTCGCGGCGCCGCGGCTCCCTCGAGGTCCCGGAGTCCCGGCGCTCCCGGCTCGCTT 420

| | |
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| PRIOR FILING DATE: 1997-11-07 | PRIOR APPLICATION NUMBER: 60/065186 |
| PRIOR FILING DATE: 1997-11-12 | PRIOR APPLICATION NUMBER: 60/065186 |
| PRIOR FILING DATE: 1997-11-12 | PRIOR APPLICATION NUMBER: 60/065846 |
| PRIOR FILING DATE: 1997-11-17 | PRIOR APPLICATION NUMBER: 60/066364 |
| PRIOR FILING DATE: 1997-11-21 | PRIOR APPLICATION NUMBER: 60/066455 |
| PRIOR FILING DATE: 1997-11-24 | PRIOR APPLICATION NUMBER: 60/066511 |
| PRIOR FILING DATE: 1997-11-24 | PRIOR APPLICATION NUMBER: 60/066770 |
| PRIOR FILING DATE: 1997-11-24 | PRIOR APPLICATION NUMBER: 60/069212 |
| PRIOR FILING DATE: 1997-12-11 | PRIOR APPLICATION NUMBER: 60/069278 |
| PRIOR FILING DATE: 1997-12-11 | PRIOR APPLICATION NUMBER: 60/069333 |
| PRIOR FILING DATE: 1997-12-11 | PRIOR APPLICATION NUMBER: 60/069699 |
| PRIOR FILING DATE: 1997-12-16 | PRIOR APPLICATION NUMBER: 60/070232 |
| PRIOR FILING DATE: 1998-01-23 | PRIOR APPLICATION NUMBER: 60/073612 |
| PRIOR FILING DATE: 1998-02-04 | PRIOR APPLICATION NUMBER: 60/074088 |
| PRIOR FILING DATE: 1998-02-09 | PRIOR APPLICATION NUMBER: 60/074092 |
| PRIOR FILING DATE: 1998-02-09 | PRIOR APPLICATION NUMBER: 60/077979 |
| PRIOR FILING DATE: 1998-03-12 | PRIOR APPLICATION NUMBER: 60/078910 |
| PRIOR FILING DATE: 1998-03-20 | PRIOR APPLICATION NUMBER: 60/079294 |
| PRIOR FILING DATE: 1998-03-25 | PRIOR APPLICATION NUMBER: 60/079665 |
| PRIOR FILING DATE: 1998-02-27 | PRIOR APPLICATION NUMBER: 60/079728 |
| PRIOR FILING DATE: 1998-03-27 | PRIOR APPLICATION NUMBER: 60/080165 |
| PRIOR FILING DATE: 1998-03-31 | PRIOR APPLICATION NUMBER: 60/081203 |
| PRIOR FILING DATE: 1998-04-05 | PRIOR APPLICATION NUMBER: 60/081229 |
| PRIOR FILING DATE: 1998-04-09 | PRIOR APPLICATION NUMBER: 60/081818 |
| PRIOR FILING DATE: 1998-04-14 | PRIOR APPLICATION NUMBER: 60/082999 |
| PRIOR FILING DATE: 1998-04-15 | PRIOR APPLICATION NUMBER: 60/083458 |
| PRIOR FILING DATE: 1998-04-29 | PRIOR APPLICATION NUMBER: 60/084633 |
| PRIOR FILING DATE: 1998-05-07 | PRIOR APPLICATION NUMBER: 60/085579 |
| PRIOR FILING DATE: 1998-05-13 | PRIOR APPLICATION NUMBER: 60/085579 |
| PRIOR FILING DATE: 1998-05-15 | PRIOR APPLICATION NUMBER: 60/085579 |

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-------------------------------------|-------------------------------|-------------------------------------|-------------------------------|-------------------------------------|-------------------------------|-------------------------------------|-------------------------------|-------------------------------------|-------------------------------|-------------------------------------|-------------------------------|-------------------------------------|-------------------------------|-------------------------------------|-------------------------------|-------------------------------------|-------------------------------|-------------------------------------|-------------------------------|-------------------------------------|--------------------------------|-------------------------------------|-------------------------------|-------------------------------------|-------------------------------|-------------------------------------|-------------------------------|-------------------------------------|-------------------------------|-------------------------------------|-------------------------------|-------------------------------------|-------------------------------|-------------------------------------|-------------------------------|-------------------------------------|-------------------------------|-------------------------------------|-------------------------------|-------------------------------------|-------------------------------|-------------------------------------|-------------------------------|-------------------------------------|-------------------------------|
| PRIOR APPLICATION NUMBER: 60/085657 | PRIOR FILING DATE: 1998-05-15 | PRIOR APPLICATION NUMBER: 60/085697 | PRIOR FILING DATE: 1998-05-15 | PRIOR APPLICATION NUMBER: 60/085704 | PRIOR FILING DATE: 1998-05-15 | PRIOR APPLICATION NUMBER: 60/086414 | PRIOR FILING DATE: 1998-05-22 | PRIOR APPLICATION NUMBER: 60/086430 | PRIOR FILING DATE: 1998-05-22 | PRIOR APPLICATION NUMBER: 60/087106 | PRIOR FILING DATE: 1998-05-28 | PRIOR APPLICATION NUMBER: 60/088026 | PRIOR FILING DATE: 1998-06-04 | PRIOR APPLICATION NUMBER: 60/088730 | PRIOR FILING DATE: 1998-06-10 | PRIOR APPLICATION NUMBER: 60/088741 | PRIOR FILING DATE: 1998-06-10 | PRIOR APPLICATION NUMBER: 60/088810 | PRIOR FILING DATE: 1998-06-10 | PRIOR APPLICATION NUMBER: 60/088858 | PRIOR FILING DATE: 19/98-06-11 | PRIOR APPLICATION NUMBER: 60/089332 | PRIOR FILING DATE: 1998-06-17 | PRIOR APPLICATION NUMBER: 60/089599 | PRIOR FILING DATE: 1998-06-17 | PRIOR APPLICATION NUMBER: 60/089907 | PRIOR FILING DATE: 1998-06-18 | PRIOR APPLICATION NUMBER: 60/089947 | PRIOR FILING DATE: 1998-06-19 | PRIOR APPLICATION NUMBER: 60/090349 | PRIOR FILING DATE: 1998-06-23 | PRIOR APPLICATION NUMBER: 60/090429 | PRIOR FILING DATE: 1998-06-24 | PRIOR APPLICATION NUMBER: 60/090455 | PRIOR FILING DATE: 1998-06-24 | PRIOR APPLICATION NUMBER: 60/090538 | PRIOR FILING DATE: 1998-06-24 | PRIOR APPLICATION NUMBER: 60/090863 | PRIOR FILING DATE: 1998-06-26 | PRIOR APPLICATION NUMBER: 60/091360 | PRIOR FILING DATE: 1998-07-01 | PRIOR APPLICATION NUMBER: 60/091519 | PRIOR FILING DATE: 1998-07-02 | PRIOR APPLICATION NUMBER: 60/091982 | PRIOR FILING DATE: 1998-07-07 |
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| | | | | |
|-----------------------|-----------------|-----------------|-----------|--------------|
| Query Match | 6.18; | Score 39.8; | DB 9; | length 1377; |
| Best Local Similarity | 56.58; | Pred. No. 0.17; | | |
| Matches 74; | Conservative 0; | Mismatches 57; | Indels 0; | Gaps 0; |

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|----|-----|---|-----|
| QY | 37 | CTCTGCGCTGCCCCCGCCCTCTGGCCCTTGAAGCCCCCCACAGCTTTCGCTGTGCTG | 96 |
| | | | |
| Db | 479 | CTCTCTCGCGCGCCGGGGTCCCTTCTGAGTGCCTCCGGCATCCCGGCTCCCGCTCGCGCTT | 420 |
| QY | 97 | TGATCCCCCAGCGCGGAGCAGGCCCCCGGCTCCGCGTCCGCTGGTGGGCCACGGCC | 156 |
| | | | |
| Db | 419 | TCTCTCCCGAGGCCCGGAGCGCGCTCGCGGCGCTGCAGGCATCGCGGCCCGGCAAGC | 360 |
| QY | 157 | CCGGTTGCCA | 167 |
| | | | |
| Db | 359 | CTTGCGTCCA | 349 |

RESULT 10
US-10-121-049-361/c

; Sequence 361, Application US/10121049
; Publication No. US20030022239A1

; GENERAL INFORMATION.

APPLICANT: Baker, Kevin P.

APPLICANT: Beresini, Maureen ;

APPLICANT: DeForge, Laura

APPLICANT: Desnoyers, Luc

APPLICANT: Filvaroff, Ellen

APPLICANT: Gao, Wei-Qiang

```

: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Sherwood, Steven
: APPLICANT: Smith, Victoria
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K
: APPLICANT: Wood, William
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P3330R1C17
: CURRENT APPLICATION NUMBER: US/10/121,049
: PRIOR APPLICATION REMOVED - See File Wrapper or Palm
: NUMBER OF SEQ ID NOS: 550
: SEQ ID NO 361
: LENGTH: 1377
: TYPE: DNA
: ORGANISM: Homo Sapien
: US-10-121-049-361

```

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Query Match          6.1%; Score 39.8; DB 9; Length 1377;
Best Local Similarity 56.5%; Pred. No. 0.17;
Matches 74; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

```

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QY 37 CTGCTGCTGCCCCCGGCGCCCTGTGAGCCCTTGAGCCCGCCAGCTTGTGCTGTGCTG 96
    || ||||| ||||| || ||||| || || ||||| || || |||||
DB 479 CTCTGTGCGGCGGCGGCGGCTCCCTCGAGGTCCCGGCGAGTCCCGGCTCCGCTGCTT 420
QY 97 TGATCCCCCAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 156
    | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 419 TCTCTCCGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360
QY 157 CCCGCTTGCCA 167
    || || |||||
DB 359 CCTGCTGCCA 349

```

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RESULT 11
US-10-123-904-361/C
: Sequence 361, Application US/10123904
: Publication No. US20030022328A1
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Beresini, Maureen
: APPLICANT: Deforge, Laura
: APPLICANT: Desnoyers, Luc
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Sherwood, Steven
: APPLICANT: Smith, Victoria
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K
: APPLICANT: Wood, William
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P3330R1C54
: CURRENT APPLICATION NUMBER: US/10/123,904
: CURRENT FILING DATE: 2002-04-16
: PRIOR APPLICATION REMOVED - See File Wrapper or Palm
: NUMBER OF SEQ ID NOS: 550
: SEQ ID NO 361
: LENGTH: 1377
: TYPE: DNA

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: ORGANISM: Homo Sapien
: US-10-123-904-361
Query Match          6.1%; Score 39.8; DB 9; Length 1377;
Best Local Similarity 56.5%; Pred. No. 0.17;
Matches 74; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

```

```

QY 37 CTGCTGCTGCCCCCGGCGCCCTGTGAGCCCTTGAGCCCGCCAGCTTGTGCTGTGCTG 96
    || ||||| ||||| || ||||| || || ||||| || || |||||
DB 479 CTCTGTGCGGCGGCGGCGGCTCCCTCGAGGTCCCGGCGAGTCCCGGCTCCGCTGCTT 420
QY 97 TGATCCCCCAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 156
    | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 419 TCTCTCCGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360
QY 157 CCCGCTTGCCA 167
    || || |||||
DB 359 CCTGCTGCCA 349

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RESULT 12
US-10-140-470-361/C
: Sequence 361, Application US/10140470
: Publication No. US20030022331A1
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Beresini, Maureen
: APPLICANT: Deforge, Laura
: APPLICANT: Desnoyers, Luc
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Sherwood, Steven
: APPLICANT: Smith, Victoria
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K
: APPLICANT: Wood, William
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P3330R1C160
: CURRENT APPLICATION NUMBER: US/10/140,470
: CURRENT FILING DATE: 2002-05-06
: PRIOR APPLICATION REMOVED - See File Wrapper
: NUMBER OF SEQ ID NOS: 550
: SEQ ID NO 361
: LENGTH: 1377
: TYPE: DNA
: ORGANISM: Homo Sapien
: US-10-140-470-361

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Query Match          6.1%; Score 39.8; DB 9; Length 1377;
Best Local Similarity 56.5%; Pred. No. 0.17;
Matches 74; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

```

```

QY 37 CTGCTGCTGCCCCCGGCGCCCTGTGAGCCCTTGAGCCCGCCAGCTTGTGCTGTGCTG 96
    || ||||| ||||| || ||||| || || ||||| || || |||||
DB 479 CTCTGTGCGGCGGCGGCGGCTCCCTCGAGGTCCCGGCGAGTCCCGGCTCCGCTGCTT 420
QY 97 TGATCCCCCAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 156
    | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 419 TCTCTCCGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360
QY 157 CCCGCTTGCCA 167
    || || |||||
DB 359 CCTGCTGCCA 349

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RESULT 13

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US-09-866-028-41/c
; Sequence 41, Application US/09866028
; Patent No. US20020058309A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Bolstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerlitsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kijavlin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/866, 028
; CURRENT FILING DATE: 2001-05-25
; Prior application data removed - consult PAM or file wrapper
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 41
; LENGTH: 1377
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-866-028-41
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Query Match 6.1%; Score 39.8; DB 10; Length 1377;
Best Local Similarity 56.5%; Pred. No. 0.17;
Matches 74; Conservative 0; Mismatches 57; Indels 0; Gaps 0;
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QY 37 CTGCTCGCTGCCCCGCGCCCTTGAGCCCTTGAGCCCCCAAGCTTCTGCTGTG 96
    || || || || || || || || || || || || || || || || || || ||
DB 479 CTCTCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTT 420
    || || || || || || || || || || || || || || || || || || ||
DB 419 TCTCTCCCGGAGCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
    || || || || || || || || || || || || || || || || || || ||
QY 157 CCGCGTGCCTCA 167
    || || || || || || || || || || || || || || || || || || ||
DB 359 CCTGCGTGCCTCA 349
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RESULT 14
US-09-944-449-41/c
; Sequence 41, Application US/09944449
; Patent No. US20020102647A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Bolstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerlitsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kijavlin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
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FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944, 449
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866, 028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067, 411
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069, 334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069, 335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069, 278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069, 425
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069, 636
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069, 694
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069, 702
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069, 870
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069, 873
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/068, 017
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/070, 440
PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/074, 086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074, 092
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075, 945
PRIOR FILING DATE: February 25, 1998
PRIOR APPLICATION NUMBER: 60/112, 850
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113, 286
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/146, 222
PRIOR FILING DATE: July 28, 1999
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: September 16, 1998
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: December 1, 1998
PRIOR APPLICATION NUMBER: 09/216, 021
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/218, 517
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254, 311
PRIOR FILING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: June 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: No. US20020102647A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: No. US20020102647A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December 1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR FILING DATE: February 11, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: May 22, 2000
```

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; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 41
; LENGTH: 1377
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-944-449-41

Query Match      6.1%; Score 39.8; DB 10; Length 1377;
Best Local Similarity 56.5%; Pred. No. 0.17;
Matches 74; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 37 CTGCTGCGCGCCCGCCGCTGCGCCCTTGAGGCCCCCAGCTTGCTGTCGCG 96
DB 479 CTCTTGCGCGCCCGCGGCTCCCTCGAGTCCGCGAGTCCGCGCTCCGCGCTT 420
QY 97 TGATCCCCCAGCGCGCGCGCGCTCGCGTCCCGCGCGCGCGCGCGCGCGCC 156
DB 419 TCTCTCCCGAGACCCCGCGCGCGCGCTCGCGCGCGCTCGCGCGCGCGCGCG 360
QY 157 CCGCGTTGCCA 167
DB 359 CCTGCGTCCCA 349

RESULT 15
US-09-944-457-41/c
; Sequence 41, Application US/09944457
; Patent No. US20020110859A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gertsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548PIC1
; CURRENT APPLICATION NUMBER: US/09/944,457
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
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; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020110859A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020110859A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 41
; LENGTH: 1377
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-944-457-41

Query Match      6.1%; Score 39.8; DB 10; Length 1377;
Best Local Similarity 56.5%; Pred. No. 0.17;
Matches 74; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 37 CTGCTGCGCGCCCGCCGCTGCGCCCTTGAGGCCCCCAGCTTGCTGTCGCG 96
DB 479 CTCTTGCGCGCCCGCGGCTCCCTCGAGTCCGCGAGTCCGCGCTCCGCGCTT 420
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OM nucleic - nucleic search, using sw model

Run on: February 9, 2003, 18:46:59 : Search time 1931 Seconds
(without alignments)
5501.936 Million cell updates/sec

Title: US-10-060-066-2

Perfect score: 656
Sequence: 1 tatgcttcacactgcacact.....tgtaattttattcttcttg 656

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST :
1: em_estbda:*
2: em_esthum:*
3: em_estlin:*
4: em_estlun:*
5: em_estlov:*
6: em_estlpl:*
7: em_estro:*
8: em_hlcc:*
9: gb_estcl:*
10: gb_estl2:*
11: gb_hlc:*
12: gb_estl3:*
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14: gb_estl5:*
15: em_estlfun:*
16: em_estlom:*
17: gb_gsa:*
18: em_gsa_hum:*
19: em_gsa_luv:*
20: em_gsa_pin:*
21: em_gsa_vrt:*
22: em_gsa_fun:*
23: em_gsa_mam:*
24: em_gsa_mus:*
25: em_gsa_other:*
26: em_gsa_pro:*
27: em_gsa_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 1 | 332.4 | 50.7 | 337 | 10 | BE647856 UI-M-BH1- |
| 2 | 234.2 | 35.7 | 558 | 14 | BQ266161 NISC-fil |
| 3 | 189.6 | 28.9 | 547 | 12 | BE102334 UI-R-BT1- |
| 4 | 174 | 26.5 | 245 | 10 | BE864111 UI-M-BH1- |
| 5 | 159.8 | 24.4 | 663 | 10 | BB641732 BB641732 |
| 6 | 155.8 | 23.8 | 472 | 10 | AM060348 UI-M-BH1- |

| 7 | 102.2 | 15.6 | 983 | 17 | CNS0489M | AL279005 Tetradon |
|----|-------|------|------|----|-----------|---------------------|
| 8 | 86.4 | 13.2 | 600 | 12 | BE6803929 | BG603929 0243-54 M |
| 9 | 81.8 | 12.5 | 594 | 13 | BT981765 | BT981765 fus0d11.y |
| 10 | 81.4 | 12.4 | 587 | 13 | BT844628 | BT844628 fql4g03.y |
| 11 | 74.4 | 11.3 | 999 | 17 | CNS04NDM | AL298579 Tetradon |
| 12 | 73.6 | 11.2 | 691 | 13 | BC912818 | BC912818 602807258 |
| 13 | 73.2 | 11.2 | 592 | 17 | FR0019468 | AL012359 F.rubripe |
| 14 | 73.2 | 11.2 | 615 | 17 | CNS04174 | AL291865 Tetradon |
| 15 | 61.4 | 9.4 | 687 | 17 | CNS0410Q | AL296459 Tetradon |
| 16 | 61.4 | 9.4 | 688 | 10 | BE212599 | BE212599 IPbrn0032 |
| 17 | 61.4 | 9.4 | 697 | 10 | BE574164 | BE574164 IPbrn0116 |
| 18 | 56 | 8.5 | 923 | 17 | CNS021DK | AL176753 Tetradon |
| 19 | 54.4 | 8.3 | 575 | 17 | FR0019451 | AL012342 F.rubripe |
| 20 | 54.4 | 8.3 | 580 | 10 | BE222518 | BE222518 hv92c08.x |
| 21 | 54.4 | 8.3 | 599 | 9 | AT912567 | AT912567 w11h12.x |
| 22 | 54.4 | 8.3 | 606 | 9 | AT680925 | AT680925 tx42h02.x |
| 23 | 54.4 | 8.3 | 640 | 10 | BE670532 | BE670532 7e37e05.x |
| 24 | 54 | 8.2 | 1043 | 17 | CNS03MBE | AL250547 Tetradon |
| 25 | 53.6 | 8.2 | 649 | 14 | BM951619 | BM951619 UI-M-EG0- |
| 26 | 53.6 | 8.2 | 855 | 13 | BT39481 | BT39481 603361722 |
| 27 | 53.4 | 8.1 | 157 | 9 | AT693801 | AT693801 w487a03.x |
| 28 | 53.4 | 8.1 | 965 | 13 | BT457751 | BT457751 603198193 |
| 29 | 52.8 | 8.0 | 477 | 12 | BE861331 | BE861331 UI-M-AK0- |
| 30 | 52 | 7.9 | 739 | 13 | BT553438 | BT553438 603193385 |
| 31 | 52 | 7.9 | 757 | 13 | BT821976 | BT821976 603039793 |
| 32 | 52 | 7.9 | 763 | 13 | BT533725 | BT533725 603028241 |
| 33 | 52 | 7.9 | 776 | 12 | BT6705097 | BT6705097 602688041 |
| 34 | 52 | 7.9 | 788 | 13 | BT456513 | BT456513 603191523 |
| 35 | 52 | 7.9 | 872 | 13 | BT1821441 | BT1821441 603038325 |
| 36 | 52 | 7.9 | 890 | 13 | BT154699 | BT154699 603242658 |
| 37 | 52 | 7.9 | 1080 | 17 | AO893056 | AO893056 HS.4832.A |
| 38 | 52 | 7.9 | 1938 | 11 | BC033741 | BC033741 Homo sapi |
| 39 | 50.8 | 7.7 | 710 | 17 | AO689558 | AO689558 nbx0079L |
| 40 | 50.4 | 7.7 | 436 | 17 | BT50198 | BT50198 CT978SK-89 |
| 41 | 49.8 | 7.6 | 776 | 17 | CNS010RY | AL099352 Drosophila |
| 42 | 49.8 | 7.6 | 844 | 17 | CNS0052P | AL056652 Drosophila |
| 43 | 49.8 | 7.6 | 887 | 14 | BQ429511 | BQ429511 AGENCOURT |
| 44 | 49.8 | 7.6 | 971 | 17 | AG079392 | AG079392 pan trogl |
| 45 | 49.6 | 7.6 | 641 | 9 | AT357868 | AT357868 qv13b02.x |

ALIGNMENTS

RESULT 1
BE647856
LOCUS
DEFINITION UI-M-BH1-anh-c-12-0-UI.r1 NIH_BMAP.M.S2 Mus musculus CDNA clone
UI-M-BH1-anh-c-12-0-UI 5', mRNA sequence.

ACCESSION BE647856
VERSION BE647856.1 GI:9973676
KEYWORDS
SOURCE EST.
ORGANISM house mouse.
Mus musculus

REFERENCE
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 9704477

COMMENT

Contact: Chn, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mestr@mail.nih.gov
CDNA Library Preparation: M.B. Soares lab Clone distribution:
Researchers may obtain BMAP CDNA clones from RESEARCH GENETICS. It
should be noted that Bento Soares is generating a small number of
additional specialized non-redundant arrays of BMAP cDNAs whose

availability will be considered under appropriate and limited collaborative arrangements. The following repetitive elements were found in this cDNA sequence: 88-148, >GC-rich#How_complexity

Seq primer: M13 Reverse.
Location/Qualifiers
1. 337

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UI-M-BM1-anh-c-12-0-UI"
/clone_lib="NIH_BMAP_M_S2"
/dev_stage="27-32 days"
/lab_host="DH10B (Life Technologies)"
/note="Vector: p7T3D-Pac (Pharmacia) with a modified polylinker. Site_1: Not I; Site_2: Eco RI; The NIH_BMAP_M_S2 library is a subtracted library derived from NIH_BMAP_M_S1, which in turn is a subtracted library derived from a mixture of normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hippocampus). The driver used for subtraction consisted of a pool of 5,000 clones from the NIH_BMAP_M_S1 library and a pool of 2,000 clones obtained from non-normalized and normalized mouse brain spinal cord libraries."

BASE COUNT 56 a 128 c 86 g 67 t
ORIGIN

Query Match 50.7%; Score 332.4; DB 10; Length 337;
Best Local Similarity 99.7%; Pred. No. 1.6e-66;
Matches 333; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 17 ACCCTGCGCTGACGACCACTGCTGCTGCCCCCGCCCTTGCGCCCTTGAGGCC 76
DB 4 ACCCTGCGCTGACGACCACTGCTGCTGCCCCCGCCCTTGCGCCCTTGAGGCC 63
OY 77 CCCACTTCTGCTGTGCTGTATCCCCCAGCCGCGGACAGCGCCCTCGCTGCC 136
DB 64 CCCACTTCTGCTGTGCTGTATCCCCCAGCCGCGGACAGCGCCCTCGCTGCC 123
OY 137 CCGGTGCTGCGCCAGCGCCCGCGGTGCGCATGAGTGAAGTGAAGTGAAGCGCTG 196
DB 124 CCGGTGCTGCGCCAGCGCCCGCGGTGCGCATGAGTGAAGTGAAGTGAAGCGCTG 183
OY 197 GATGAAGAGAGGGGCTTGTGTGTGAAGAGGGGCTTGAAGTGAAGTGAAGCGCTG 256
DB 184 GATGAAGAGAGGGGCTTGTGTGTGAAGAGGGGCTTGAAGTGAAGTGAAGCGCTG 243
OY 257 CCGCTTGGCGGCTTGTGCTGATGACCATGCGCATGAGTGAAGTGAAGCGCTG 316
DB 244 CCGCTTGGCGGCTTGTGCTGATGACCATGCGCATGAGTGAAGTGAAGCGCTG 303
OY 317 AAGAGCTCATCTGCAACACCAACCACTCACA 350
DB 304 AAGAGCTCATCTGCAACACCAACCACTCACA 337

RESULT 2
LOCUS B0266161 558 bp mRNA linear EST 07-MAY-2002
DEFINITION NISC_ff11c05.x1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:2865416
ACCESSION B0266161
VERSION B0266161.1 GI:20491226
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 558)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL
COMMENT

Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen/Robin Humphreys
cDNA Library Preparation: Life Technologies
cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC)
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
info@image.llnl.gov
WGI:1046188

FEATURES
source
Seq primer: -21M13 forward primer (ABI).
Location/Qualifiers
1. 558

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:2865416"
/clone_lib="NCI_CGAP_Mam5"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"

BASE COUNT 153 a 152 c 131 g 122 t
ORIGIN

Query Match 35.7%; Score 234.2; DB 14; Length 558;
Best Local Similarity 89.2%; Pred. No. 6.9e-44;
Matches 256; Conservative 0; Mismatches 30; Indels 1; Gaps 1;

OY 370 CCCATCGTGGGGGCGAGTGGCTCTCCGAGAGAGAGACCTGGGGGCTCAGACATTAG 429
DB 558 CCCATCGTGGGGGCGAGTGGCTCTCCGAGAGAGAGACCTGGGGGCTCAGACATTAG 499
OY 430 GCCTTGCGGATATGCTGCTGCGAGTGAAGGTGAGAGAGCCCTGGCGCCACTGC 489
DB 498 GCCTTGCGGATATGCTGCTGCGAGAGTGAAGGTGAGAGAGCCCTGGCGCCACTGC 439
OY 490 CGNTGAAGCGTGTGCTTCAGCAATTCAGTCTTGTGACTCTCAACCCAAAGGNC 549
DB 438 CGCTGAAGCGTGTGCTTCAGCAATTCAGTCTTGTGACTCTCAACCCAAAGGNC 379
OY 550 TTGAGGGGTGTGCTTACTGCTGAGAGGGGAGNTATTCATGACCCCTCCATNCTNT 609
DB 378 TTGATGGGTGTGCTTACTGCTGAGAGGGGAGNTATTCATGACCCCTCCATNCTNT 319
OY 610 ACAATCCCTCTTCTGGGAGTTNTGNTATTATTTATTTATTTCTTGG 656
DB 318 -CAATCCCTCTTCTGGGAGTTCTGTTATTTATTTATTTATCTAG 273

RESULT 3
LOCUS BE102334 547 bp mRNA linear EST 13-JUN-2000
DEFINITION UT-R-BT1-aql-d-02-0-UI s1 UT-R-BT1 Rattus norvegicus cDNA clone
ACCESSION BE102334
VERSION BE102334.1 GI:8494433
KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
1 (bases 1 to 547)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene

JOURNAL
MEDLINE
COMMENT

discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized corpus striatum library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) The following repetitive elements were found in this cDNA sequence: 147-294, >B3MSINE/B2
Seq primer: M13 Forward
POLYA=yes.

FEATURES
SOURCE

Location/Qualifiers
1. 347
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="ur-R-BT1-aq1-d-02-0-UI"
/clone_1lb="UI-R-BT1"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker: Site.1: Not I; Site.2: Eco RI; The library ur-R-BT1 is a subtracted library derived from a mixture of the following tissues: hippocampus, thalamus, mid-brain, medulla, corpus striatum, cerebral cortex and testis. For a detailed description of the library from which this clone was derived, please visit our web site at retest.eng.uiowa.edu. The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
TAG_LIB=UI-R-BT1
TAG_TISSUE=corpus-striatum
TAG_SEQ=CTAGG"

BASE COUNT 150 a 148 c 121 g 128 t

ORIGIN

Query Match 28.9%; Score 189.6; DB 10; Length 547;
Best Local Similarity 90.5%; Pred. No. 1.3e-33;
Matches 209; Conservative 0; Mismatches 21; Indels 1; Gaps 1;

QY 375 CGTGGGCGACTGCTCTCCGAGAGAGAGACCTGGGGCCACACATTCAGGCTC 434
|||||
Db 547 CGTGGGCGACTGCTCTCCGAGAGAGAGACCTGGGGCCACACATTCAGGCTC 488
|||||
QY 435 TGGGGGATATGCTGCGAGAGAGGCTGCGAGAGGCTGCGCCACCTCCGCTG 494
|||||
Db 487 TGGGGGATATGCTGCGAGAGAGGCTGCGAGAGGCTGCGCCACCTCCGCTG 428
|||||
QY 495 AAGCCTGTGCTCAGCAATCGACTTATAGTCTTGAGTCTCAACCAAGAGCTTGAG 554
|||||
Db 427 AAGCCTGTGCTCAGCAATCGACTTATAGTCTTGAGTCTCAACCAAGAGCTTGAG 368
|||||
QY 555 GGGTGTGCTTACTGCTGAGAGCG-GGTTNATTCATGACCCCTCCATNCC 604
|||||
Db 367 GGGTGTGCTTACTGCTGAGAGCG-GGTTNATTCATGACCCCTCCATNCC 317
|||||

RESULT 4
BE864111/c 245 bp mRNA linear EST 29-SEP-2000
LOCUS BE864111
DEFINITION UI-M-BH1-amp-a-08-0-UI.r1 NIH_BMAP_M_S2 Mus musculus cDNA clone
ACCESSION BE864111
UI-M-BH1-amp-a-08-0-UI 5', mRNA sequence.

VERSION
KEYWORDS
SOURCE
ORGANISM

BE864111.1 GI:10384829
EST.
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 245)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: m8st@mail.nih.gov

JOURNAL
MEDLINE
COMMENT

Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements
Seq primer: M13 Reverse.

FEATURES
SOURCE

Location/Qualifiers
1. 245
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="ur-M-BH1-amp-a-08-0-UI"
/clone_1lb="NIH_BMAP_M_S2"
/dev_stage="27-32 days"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker: Site.1: Not I; Site.2: Eco RI; The NIH_BMAP_M_S2 library is a subtracted library derived from NIH_BMAP_M_S1, which in turn is a subtracted library derived from a mixture of normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hippocampus). The driver used for subtraction consisted of a pool of 5,000 clones from the NIH_BMAP_M_S1 library and a pool of 2,000 clones obtained from non-normalized and normalized mouse brain spinal cord libraries."

BASE COUNT 39 a 67 c 77 g 61 t 1 others

ORIGIN

Query Match 26.5%; Score 174; DB 12; Length 245;
Best Local Similarity 99.4%; Pred. No. 5.3e-30;
Matches 174; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 283 CCATCGCATAGACGACGACTACTGCTCTACACAAAGCTCTGATCGCAACACCA 342
|||||
Db 245 CCATCGCATAGACGACGACTACTGCTCTACACAAAGCTCTGATCGCAACACCA 186
|||||
QY 343 ACCCTACAGCAGGATGATGACGACACCCATCTGGGGGAGATGGCTCTCCGAGA 402
|||||
Db 185 ACCCTACAGCAGGATGATGACGACACCCATCTGGGGGAGATGGCTCTCCGAGA 126
|||||
QY 403 AGGACCTGGGGGCTTCACACATTCAGGCTCTGGGGGATATGCTGCTGGAAG 457
|||||
Db 125 AGGACCTGGGGGCTTCACACATTCAGGCTCTGGGGGATATGCTGCTGGAAG 71
|||||

RESULT 5
BB641732 663 bp mRNA linear EST 26-OCT-2001
LOCUS BB641732
DEFINITION BB641732 RIKEN full-length enriched, 10 days neonate cortex Mus
ACCESSION BB641732
musculus cDNA clone AB30045A22 5', mRNA sequence.

| VERSION | BB641732.1 | GI:16476827 |
|-----------|--|-------------|
| KEYWORDS | EST. | |
| SOURCE | house mouse. | |
| ORGANISM | Mus musculus | |
| REFERENCE | Eukaryotic: Metazoa: Chordata: Craniata: Vertebrata; Euteleostomi: Mammalia, Eutheria, Rodentia; Sciurognathi, Muridae; Mus. 1 (bases 1 to 663) | |
| AUTHORS | Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Horii,F., Ishii,Y., Ito,M., Kawai,T., Komno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shingawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takehashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y. | |
| TITLE | RIKEN Mouse ESTs (Arakawa,T., et al. 2001) | |
| JOURNAL | Unpublished (2001) | |
| COMMENT | Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suenhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gsc.riken.go.jp, url:http://genome.gsc.riken.go.jp/ Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Komno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) wag1,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Matsuhiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,T., Okazaki,Y., Muramatsu,M., Inoue,Y., Kiria,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Komno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y. Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shingawa,A., Saito,T., Kiyosawa,H., Yamanake,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y. Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details. e mouse tissues. | |
| FEATURES | Location/Qualifiers | |
| Source | 1. 663 /organism="Mus musculus" /db_xref="taxon:10090" /clone="AB30045A22" /clone_lfp="RIKEN full-length enriched, 10 days neonate cortex" /tissue_type="cortex" /dev_stage="10 days neonate" /lab_host="DH10B" /note="Site_1: Sali; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGGAGAGAGGATCCAGAGGCTCTTTTCTTTTCTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of | |

[illegible]


```
/organism="Mus musculus"
/db_xref="C57BL/6J"
/clone="UI-M-BH1-abh-c-12-0-UI"
/dev_stage="27-32 days"
/lab_host="DH10B (Life Technologies)"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker. Site 1: Not I; Site 2: Eco RI; The
NIH-BMAP_M_S2 library is a subtracted library derived from
NIH-BMAP_M_S1, which in turn is a subtracted library
derived from a mixture of normalized libraries from ten
regions of the mouse brain (cerebellum, brain stems,
olfactory bulbs, hypothalamus, cortex, amygdala, basal
ganglia, pineal gland, striatum, hippocampus). The driver
used for subtraction consisted of a pool of 5,000 clones
from the NIH-BMAP_M_S1 library and a pool of 2,000 clones
obtained from non-normalized and normalized mouse brain
spinal cord libraries.
TAG_LIB=NIH-BMAP_M_S2
TAG_TISSUE=hypothalamus
TAG_SEQ=CGGTA

BASE COUNT      138 a      125 c      106 g      103 t
ORIGIN
Query Match      23.8%; Score 155.8; DB 10; Length 472;
Best Local Similarity 85.5%; Pred. No. 8.1e-26;
Matches 177; Conservative 0; Mismatches 29; Indels 1; Gaps 1;

QY 450 CTGGAAGTAGGCTGACAGAGAGCCCTGGCTGCACCTCCGCTGAGAGCTGTGCTTCA 509
      |||||||  |||  |||||  |||  |||||  |||  |||||  |||  |||||  |||
DB 472 CTGGAAGTAGGCTGACAGAGAGCCCTGGCTGCACCTCCGCTGAGAGCTGTGCTTCA 413
      |||||||  |||  |||||  |||  |||||  |||  |||||  |||  |||||  |||

QY 510 GCAAAATGACCTTNTAGTGTCTGAGTCTCAACCAAGGCTTGAGGGGTGCTTTACTG 569
      |||||||  |||  |||||  |||  |||||  |||  |||||  |||  |||||  |||
DB 412 GCAAAATGACCTTNTAGTGTCTGAGTCTCAACCAAGGCTTGAGGGGTGCTTTACTG 353
      |||||||  |||  |||||  |||  |||||  |||  |||||  |||  |||||  |||

QY 570 CTGAGAGCGGCTNTATCATGACACCCCTCCATNCTNTATCAAAATCCCTCTTCTGGGGA 629
      |||||||  |||  |||||  |||  |||||  |||  |||||  |||  |||||  |||
DB 352 CTGAGAGCGGCTNTATCATGACACCCCTCCATNCTNTATCAAAATCCCTCTTCTGGGAT 294
      |||||||  |||  |||||  |||  |||||  |||  |||||  |||  |||||  |||

QY 630 TTNTNGNTGATTTATTTATTTCTTTG 656
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 293 TCTGCTTTATTTATTTATTTACTGG 267
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

* RESULT 7
CNS0489W      983 bp      DNA      linear      GSS 19-MAY-2000
LOCUS      Tetraodon nigroviridis genome survey sequence T7 end of clone
DEFINITION      090G15 of library G from Tetraodon nigroviridis, genomic survey
sequence.
ACCESSION      AL279005.1 GI:8016339
VERSION      AL279005.1
KEYWORDS      GSS: genome survey sequence.
SOURCE      Tetraodon nigroviridis.
ORGANISM      Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
1 (bases 1 to 983)
Roest-Criollus, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brothier, P., Quetier, F.,
Saurin, W., and Weissenbach, J.
Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
Unpublished
2 (bases 1 to 983)
Roest-Criollus, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.,
Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A., and
Weissenbach, J.
Characterization and repeat analysis of the compact genome of the

/organism="Mus musculus"
/db_xref="C57BL/6J"
/clone="UI-M-BH1-abh-c-12-0-UI"
/dev_stage="27-32 days"
/lab_host="DH10B (Life Technologies)"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker. Site 1: Not I; Site 2: Eco RI; The
NIH-BMAP_M_S2 library is a subtracted library derived from
NIH-BMAP_M_S1, which in turn is a subtracted library
derived from a mixture of normalized libraries from ten
regions of the mouse brain (cerebellum, brain stems,
olfactory bulbs, hypothalamus, cortex, amygdala, basal
ganglia, pineal gland, striatum, hippocampus). The driver
used for subtraction consisted of a pool of 5,000 clones
from the NIH-BMAP_M_S1 library and a pool of 2,000 clones
obtained from non-normalized and normalized mouse brain
spinal cord libraries.
TAG_LIB=NIH-BMAP_M_S2
TAG_TISSUE=hypothalamus
TAG_SEQ=CGGTA

BASE COUNT      138 a      125 c      106 g      103 t
ORIGIN
Query Match      23.8%; Score 155.8; DB 10; Length 472;
Best Local Similarity 85.5%; Pred. No. 8.1e-26;
Matches 177; Conservative 0; Mismatches 29; Indels 1; Gaps 1;

QY 450 CTGGAAGTAGGCTGACAGAGAGCCCTGGCTGCACCTCCGCTGAGAGCTGTGCTTCA 509
      |||||||  |||  |||||  |||  |||||  |||  |||||  |||  |||||  |||
DB 472 CTGGAAGTAGGCTGACAGAGAGCCCTGGCTGCACCTCCGCTGAGAGCTGTGCTTCA 413
      |||||||  |||  |||||  |||  |||||  |||  |||||  |||  |||||  |||

QY 510 GCAAAATGACCTTNTAGTGTCTGAGTCTCAACCAAGGCTTGAGGGGTGCTTTACTG 569
      |||||||  |||  |||||  |||  |||||  |||  |||||  |||  |||||  |||
DB 412 GCAAAATGACCTTNTAGTGTCTGAGTCTCAACCAAGGCTTGAGGGGTGCTTTACTG 353
      |||||||  |||  |||||  |||  |||||  |||  |||||  |||  |||||  |||

QY 570 CTGAGAGCGGCTNTATCATGACACCCCTCCATNCTNTATCAAAATCCCTCTTCTGGGGA 629
      |||||||  |||  |||||  |||  |||||  |||  |||||  |||  |||||  |||
DB 352 CTGAGAGCGGCTNTATCATGACACCCCTCCATNCTNTATCAAAATCCCTCTTCTGGGAT 294
      |||||||  |||  |||||  |||  |||||  |||  |||||  |||  |||||  |||

QY 630 TTNTNGNTGATTTATTTATTTCTTTG 656
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 293 TCTGCTTTATTTATTTATTTACTGG 267
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

* RESULT 8
BG803929      600 bp      mRNA      linear      EST 20-DEC-2001
LOCUS      Bg803929
DEFINITION      0243-54 Mouse E14.5 retina lambda ZAP II library Mus musculus cDNA,
mRNA sequence.
ACCESSION      BG803929
VERSION      BG803929.1 GI:17950842
KEYWORDS      EST.
SOURCE      house mouse.
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 600)
Mu, X., Zhao, S., Pershad, R., Hsieh, T.-F., Scarpa, A., Wang, S. M.,
White, R. A., Beremand, P. D., Thomas, T. L., Gan, L., and Klein, W. H.
Gene expression in the developing mouse retina by EST sequencing
and microarray analysis
Nucleic Acids Res. 29 (24), 4983-4993 (2001)
Contact: Klein WH
Department of Biochemistry and Molecular Biology
University of Texas M.D. Anderson Cancer Center
Box 117, 1515 Holcombe Blvd., Houston, TX 77030, USA
Tel: 713 792 3646
Fax: 713 790 0329.
Location/Qualifiers
1..600
/organism="Mus musculus"

JOURNAL      Unpublished
REFERENCE      3 (bases 1 to 983)
AUTHORS      Genoscope.
TITLE      Direct Submission
JOURNAL      Submitted (12-APR-2000)
COMMENT      This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
Location/Qualifiers
1..983
/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="090G15"
/clone_lib="G"
/notes="Genoscope sequence ID : COBG090AD08LPI-end : T7"

BASE COUNT      216 a      305 c      254 g      202 t      6 others
ORIGIN
Query Match      15.6%; Score 102.2; DB 17; Length 983;
Best Local Similarity 67.5%; Pred. No. 1.8e-13;
Matches 168; Conservative 0; Mismatches 63; Indels 18; Gaps 1;

QY 214 TGTGCTGTAAGAGGCGCTTCAGTACTAGTACCATGCGGCGGCTTCGGGCTTTTG 273
      |||||||  |||  |||||  |||  |||||  |||  |||||  |||  |||||  |||
DB 293 TGTGCTGAGAGCGGCGCATCCAGGTGCTGTACCATGAGACGCTTTCAGAGCTTTCG 352
      |||||||  |||  |||||  |||  |||||  |||  |||||  |||  |||||  |||

QY 274 GCTCTATGACCATGCGCATTCAGTACTGACTGTGCTTACACAGAGACTCTCATCTGCA 333
      |||||||  |||  |||||  |||  |||||  |||  |||||  |||  |||||  |||
DB 353 CCTGATATAGCGGTGGCATTCGACACGACTACTGCTGTAGCTGGCGCTTCATCTGCA 412
      |||||||  |||  |||||  |||  |||||  |||  |||||  |||  |||||  |||

QY 334 ACACCACCACTTACACAGAGTATGACGAGACCAACCCATGTGGGCGAGTGCTCT 393
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 413 ACAGACGCGCAACTCCACCCAGAGAGCAGC-----TCCAAAGCAACA 454
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY 394 CCGAAGAAAGAGACCTCGGGGCGCTCACACATTCAGGCTCGGGATGATGCTGCG 453
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 455 AAGACAAAGAGACCCCGGGGCGCTCACACATTCAGGCTCGGGATGATGCTGCG 514
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY 454 AAGTAGAG 462
      |||||  ||
DB 515 AAGTAGAG 523
      |||||  ||

* RESULT 8
BG803929      600 bp      mRNA      linear      EST 20-DEC-2001
LOCUS      Bg803929
DEFINITION      0243-54 Mouse E14.5 retina lambda ZAP II library Mus musculus cDNA,
mRNA sequence.
ACCESSION      BG803929
VERSION      BG803929.1 GI:17950842
KEYWORDS      EST.
SOURCE      house mouse.
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 600)
Mu, X., Zhao, S., Pershad, R., Hsieh, T.-F., Scarpa, A., Wang, S. M.,
White, R. A., Beremand, P. D., Thomas, T. L., Gan, L., and Klein, W. H.
Gene expression in the developing mouse retina by EST sequencing
and microarray analysis
Nucleic Acids Res. 29 (24), 4983-4993 (2001)
Contact: Klein WH
Department of Biochemistry and Molecular Biology
University of Texas M.D. Anderson Cancer Center
Box 117, 1515 Holcombe Blvd., Houston, TX 77030, USA
Tel: 713 792 3646
Fax: 713 790 0329.
Location/Qualifiers
1..600
/organism="Mus musculus"
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| BASE COUNT | 108 a | 208 c | 182 g | 102 t |
|--|---|---|-----------|-------------|
| Query Match | 13.2% | Score 86.4; | DB 12; | Length 600; |
| Best Local Similarity | 66.8%; | Pred. No. 7.9e-10; | | |
| Matches 123; | Conservative 0; | Mismatches 61; | Indels 0; | Gaps 0; |
| <p> /db_xref="taxon:10090" /clone_lib="Mouse E14.5 retina lambda ZAP II library" /tissue_type="neural retina" /dev_stage="embryonic day 14.5 post-fertilization" /notes="vector: pAMP10 (Gibco); Cloned unidirectionally. Primer: Oligo dT. RNA Isolation: cytoplasmic RNA preps (Mannatis); Cloning Technique: cDNA Cloning (Clontech, Life Technologies); Average insert size: 1.8 kb; Insertion site: TACCTCCACGTGATTCGAGG-->. Other information regarding entire library may be found at http://pga.smed.edu/Data/libraries/microarray_cdna_library ies.htm." </p> | | | | |
| OY | 214 | TGTGTGTGAAAAGGCGCTTACGCTACCTACCTACACACATGGCGCCCTTTCGCGCTTTG | 273 | |
| Db | 91 | TTCGATGGACCCGCGGTGCGAGTGCCTGACACAGCGCGACCTTTCGCGCGCTTCT | 150 | |
| *OY | 274 | GCCTATACCATCTGCATCCATCAGCTGACTGCTGCTCTACACAGAGCTCATCTGCA | 333 | |
| Db | 151 | CGCTATATGGCATCTGCCCATCGCACCGACTACTGCTGTACTCCAGCGCGCATCTGCA | 210 | |
| OY | 334 | ACACCGACCAACCTCAGACGAGTATGACGACACCCCATGTCGGGGGCACTGCTCCT | 393 | |
| Db | 211 | ACGGACCAACCTGACATGAGCAGCGGCGCCCGCGCGCTGCGCGCGACCTCA | 270 | |
| OY | 394 | CCGA | 397 | |
| Db | 271 | CCCA | 274 | |
| RESULT 9 | | | | |
| LOCUS | B1981765 | 594 bp | mRNA | linear |
| DEFINITION | fu50d11.y1 zebrafish adult brain Danio rerio cDNA clone 5333036 5' | | | |
| ACCESSION | B1981765 | | | |
| VERSION | B1981765.1 | GI:16370697 | | |
| KEYWORDS | EST. | | | |
| SOURCE | zebrafish. | | | |
| ORGANISM | Danio rerio | | | |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio. 1 (bases 1 to 594) | | | |
| AUTHORS | Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy S., Hillier,L., Kuehnb,T., Martin,D., Beck,C., Wyllie,T., Underwood R., Stepien,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shih,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R. | | | |
| TITLE | Washu zebrafish EST Project 1998 | | | |
| JOURNAL | Unpublished (1998) | | | |
| COMMENT | Other ESTs: fu50d11.x1 Contact: Stephen L. Johnson Washington University School of Medicine 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: zbrafish@watson.wustl.edu cDNA Library Preparation: John Nhai. cDNA Library Arrayed by: Matthew Clark. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: Genome Systems, St. Louis, Missouri (web address: www.genomesystems.com) (email contact: info@genomesystems.com) and Research Genetics, Huntsville, Alabama (web address: www.resgen.com) (email contact: info@resgen.com) and ResonanceZentrumPrimateDatenbank, Berlin, Germany (web address: www.rzpd.de) | | | |

| FEATURES | source | seq primer: T7 | High quality sequence stop: 438. |
|--|---|----------------|----------------------------------|
| Location/Qualifiers | 1. 594 | | |
| /organism="Danio rerio" | | | |
| /db_xref="taxon:7955" | | | |
| /clone="533036" | | | |
| /clone_lib="zebrafish adult brain" | | | |
| /sex="mixed male and female" | | | |
| /tissue_type="brain" | | | |
| /dev_stage="adult" | | | |
| /lab_host="E. coli DH10B" | | | |
| /note="Vector: pZiPlox; site_1: NotI; site_2: SalI; Original library was constructed in lambdaZiPlox. Mass excision of the cDNA library was performed to yield pZiPlox plasmids. Insert check was done in original library." | | | |
| BASE COUNT | 167 a 136 c 147 g 144 t | | |
| ORIGIN | | | |
| Query Match | 12.5%; Score 81.8; DB 13; Length 594; | | |
| Best Local Similarity | 67.1%; Pred. No. 9.1e-09; | | |
| Matches 116; Conservative | 0; Mismatches 57; Indels 0; Gaps 0; | | |
| QY | 186 TTGAACCCCTGANTGAAGAGAGGGGTTTGCTGTGTGAAGAGGCGCTCAGGTCTACTG 245 | | |
| Db | 421 TTGAAGGACACAAACCTGCCCTGCAGGATGGTGTGTGAAGAGGATTCACATCTCTCTC 480 | | |
| QY | 246 ACCACCATCGCGCGGCTTCGCGGCTTTGGAGCTTCATGACCATCGGCATCAGCATGACTAC 305 | | |
| Db | 481 ACCATCGGGGTGCATTCGTCATCTCTTGGCTGTGATGACGGTGGCTATCGGCATGATTAAC 540 | | |
| QY | 306 TGGCTTACACAGAGCTCTCATCTGACACACACCAACCTCAGACGAGTGA 358 | | |
| Db | 541 TGGCTGTACTCGCGGCGCTCATCTGCACACACCGCCACACACACACAGAGA 593 | | |
| RESULT 10 | | | |
| LOCUS | BI844628 | | |
| DEFINITION | BI844628 587 bp mRNA linear EST 26-JUL-2002 | | |
| ACCESSION | BI844628 | | |
| VERSION | BI844628.1 GI:15957151 | | |
| KEYWORDS | EST. | | |
| SOURCE | zebrafish. | | |
| ORGANISM | Danio rerio | | |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio. | | |
| AUTHORS | 1 (bases 1 to 587) | | |
| | Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Maria,M., Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,B., Gibbons,M., Page,D., Harvey,N., Schuck,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R. | | |
| TITLE | Mashu zebrafish EST Project 1998 | | |
| JOURNAL | Unpublished (1998) | | |
| COMMENT | Contact: Stephen L. Johnson Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: zbrafish@watson.wustl.edu CDNA Library Preparation: John Ngai. cDNA Library Arrayed by: Matthew Clark. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: Genome Systems, St. Louis, Missouri (web address: www.genomesystems.com) (email contact: info@genomesystems.com) and Research Genetics, Huntsville, Alabama (web address: www.resgen.com) (email contact: info@resgen.com) and Ressource@zentrumprimatdatenbank, Berlin, Germany (web address: www.tzpd.de) | | |

This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at

| ORIGIN | |
|-------------|--------------------------------------|
| Query Match | 11.28; Score 73.6; DB 13; Length 691 |

DEFINITION Tetraodon nigroviridis genome survey sequence PUC-Orig end of clone
119E09 of library G from Tetraodon nigroviridis, genomic survey
sequence.
ACCESSION AL296459.1 GI:8035039
VERSION AL296459.1
KEYWORDS GSS; genome survey sequence.
SOURCE Tetraodon nigroviridis.
ORGANISM Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
1 (bases 1 to 687)
REFERENCE Roest-Crollius, H., Jallion, O., Dasilva, C., Bouneau, L., Fisher, C.,
AUTHORS Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W., and Weissenbach, J.
Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
Unpublished
2 (bases 1 to 687)
REFERENCE Roest-Crollius, H., Jallion, O., Dasilva, C., Fizames, C., Fisher, C.,
AUTHORS Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A., and
Weissenbach, J.
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
Unpublished
3 (bases 1 to 687)
REFERENCE Genoscope.
AUTHORS Direct Submission
TITLE Submitted (12-APR-2000)
JOURNAL This sequence is a single read and was generated as part of a large
COMMENT scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
Location/Qualifiers
FEATURES
source
1. 687
/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone_1lb="G"
/note="Genoscope sequence ID : COBG119AC05SP1-end :
PUC-Orig"

BASE COUNT 154 a 152 c 207 g 155 t 19 others
ORIGIN

1 Query Match 9.4% Score 61.4; DB 17; Length 687;
Best Local Similarity 66.4%; Pred. No. 0.00045;
Matches 83; Conservative 3; Mismatches 39; Indels 0; Gaps 0;

OY 218 GTGTGAAGAAGGCGCTTGACGACTACGACCATGCGCGCTTTGGGCTT 277
|||
Db 156 GTTGACCGCGGAGTGCGAGTCGAMCAGTCGGCGCTTGCGGCTTCAGGCT 215
|||
OY 278 CATGACCATCGCATGACTGACTGACTGCTACACAGAGAGCTTCATCTGCAACAC 337
|||||
Db 216 CATGACCATCGCGTGGGAGAGACTGCTGCTACTCGCGGGGTGTGCAGAGACCA 275
|||
OY 338 CACCA 342
|||
Db 276 GGCCA 280

Search completed: February 9, 2003, 20:08:49
Job time : 1938 secs

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